

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 03:14:08 ; Search time 7483 Seconds  
(without alignments)  
4118.337 Million cell updates/sec

Title: US-10-088-950A-1  
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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	2438	9 BC028003	BC028003 Homo sapi
2	3498	100.0	2646	6 AX114318	AX114318 Sequence
3	3498	100.0	2663	6 AR022524	AR022524 Sequence
4	3498	100.0	2663	6 AR099897	AR099897 Sequence

#### ALIGNMENTS

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BC028003	BC028003	Homo sapiens interleukin 27 receptor, alpha, mRNA (cDNA clone MGC:39984 IMAGE:5212139), complete cds.	BC028003	BC028003.1	GI:20380120	MGC.	Homo sapiens (human)	1 (bases 1 to 2438)	
							Homo sapiens		
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
							1 (bases 1 to 2438)		
							Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,J.S., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,		

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2438)  
Strausberg, R.  
Direct Submission  
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-x@mail.nih.gov](mailto:cgabs-x@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hri.nih.gov](mailto:nisc_mgc@hri.nih.gov)  
Akhtar, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bonifant, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Gouffard, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, O.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Young, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
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RESULT 2

AX114318

LOCUS AX114318 2646 bp DNA linear PAT 11-MAY-2001

DEFINITION Sequence 3 from Patent WO0129070.

ACCESSION AX114318

VERSION AX114318.1 GI:14031282  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS de Sauvage, F.J., Grewal, I. and Gurney, A.L.  
 TITLE Type I cytokine receptor tccr  
 JOURNAL Patent: WO 0129070-A 3 26-APR-2001;  
 Genentech, Inc. (US)  
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ACCESSION AR022524
VERSION AR022524.1 GI:3976586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2663)
AUTHORS Baumgartner, J.W., Foster, D.C., Grant, F.J. and Sprecher, C.A.
TITLE Hematopoietic cytokine receptor
JOURNAL Patent: US 5792850-A 4 11-AUG-1998;
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2663)
AUTHORS Baumgartner,J.W., Foster,D.C., Grant,F.J. and Sprecher,C.A.
TITLE Hematopoietic cytokine receptor
JOURNAL Patent: US 6080406-A 4 27-JUN-2000;
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 AUTHORS Schreder, C.A., Grant, F.J., Baumgartner, J.W., Presnell, S.R.,  
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 Foster, D.F.  
 TITLE Cloning and characterization of a novel class I cytokine receptor  
 JOURNAL Biochem. Biophys. Res. Commun. 246 (1), 82-90 (1998)  
 MEDLINE 98262921  
 PUBMED 9600072  
 REFERENCE 2 (bases 1 to 2663)  
 AUTHORS Schreder, C.A., Grant, F.J., Baumgartner, J.W., Presnell, S.R.,  
 Schreder, S.K., Yamagiwa, T., Whitmore, T.E., O'Hara, P.J. and  
 Foster, D.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-1998) Biomolecular Informatics, ZymoGenetics,  
 Inc., 1201 Eastlake Ave. E., Seattle, WA 98102, USA  
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## Alignment Scores:

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Pred. No.: 5.89e-147 Length: 2663  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2677)
AUTHORS Zhang, W., Wan, T., He, L., Yuan, Z. and Cao, X.
TITLE A novel gp130-like cytokine receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2677)
AUTHORS Zhang, W., Wan, T., He, L., Yuan, Z. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1998) Department of Immunology, Shanghai
Brilliance Biotechnology Institute & Second Military Medical
University, 800 Xiangyin Road, Shanghai 200433, P.R. China
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 1 (bases 1 to 2628)  
 Chen, Q., Ghilardi, N., Wang, H., Baker, T., Xie, M.H., Gurney, A.,  
 Grewal, I.S. and de Sauvage, F.J.  
 Development of Th1-type immune responses requires the type I  
 cytokine receptor TCCR  
 NATURE 407 (6806), 916-920 (2000)  
 JOURNAL MEDLINE 20509354  
 PUBMED 11057672  
 REFERENCE 2 (bases 1 to 2628)  
 AUTHORS Chen, Q., Ghilardi, N., Wang, H., Xie, M.-H., Gurney, A., Grewal, I.S.

and de Sauvage, F.J.  
 Direct Submission  
 Submitted (08-MAY-2000) Molecular Oncology, Genentech Inc., 1 DNA  
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REFERENCE 1 (bases 1 to 2646)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBLISHED 12975309
REFERENCE 2 (bases 1 to 2646)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Db	712	GGCTACAAAGTGTATGGCCGTGCGGATGAGAAAGAGAGATTGTGGGGCGAGTGG 771
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
Db	772	AGCCCCATTTTGTCTTCCAGACACCGCCCTCTCTGCTCCAAAAGATGTGTGGGTATCAGGG 831
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Qy	261	CysValGlnValSerTyxLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280

Db	892	TGCTGTGAGGTGAGCTACAAAAGTCTGTGTTCTGGGTGTGGAGGTCTGTGAGTCCAGAA 951
Qy	281	GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
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Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
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Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
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Qy	381	GlyAsnPheThrValGlyValProTyxArgIleThrValThrAlaValSerAlaSerGly 400
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Qy	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
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Qy	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
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Qy	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyxThrLeuCysAlaGlnSerGlyThr 460
Db	1432	CCAAGGACCAAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGATGGAACT 1491
Qy	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
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Qy	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
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Qy	561	ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
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Qy	581	GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600
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DEFINITION Sequence 8965 from Patent WO02068579.
ACCESSION CQ723031
VERSION CQ723031.1 GI:42283888
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 8965 06-SEP-2002;
PE Corporation (NY) (US)
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Score: 3491.00 Matches: 635
Percent Similarity: 99.84% Conservative: 0
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DB: 6 Gaps: 0
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QY 41 CysTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
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RESULT 10
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DEFINITION Sequence 2 from patent US 5792850.
ACCESSION AR022523
VERSION AR022523.1 GI:3976585
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2368)
AUTHORS Baumgartner, J.W., Foster, D.C., Grant, F.J. and Sprecher, C.A.
TITLE Hematopoietic cytokine receptor
JOURNAL Patent: US 5792850-A 2 11-AUG-1998;
FEATURES
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Best Local Similarity: 90.88% Mismatches: 0
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US-10-088-950A-1 (1-636) x AR022523 (1-2368)
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DEFINITION Sequence 2 from patent US 6080406.
ACCESSION AR099896
VERSION AR099896.1 GI:12810344
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2368)
AUTHORS Baumgartner,J.W., Foster,D.C., Grant,F.J. and Sprecher,C.A.
TITLE Hematopoietic cytokine receptor
JOURNAL Patent: US 6080406-A 2 27-JUN-2000;
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US-10-088-950A-1 (1-636) x AR099896 (1-2368)

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VERSION AF053005.1 GI:3153242
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ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2586)
AUTHORS Sprecher,C.A., Grant,F.J., Baumgartner,J.W., Presnell,S.R.,
Schrader,S.K., Yamagiwa,T., Whitmore,T.E., O'Hara,P.J. and
Foster,D.F.
TITLE Cloning and characterization of a novel class I cytokine receptor
JOURNAL Blochem. Biophys. Res. Commun. 246 (1), 82-90 (1998)
MEDLINE 98262921
PUBMED 9600072
REFERENCE 2 (bases 1 to 2586)
AUTHORS Sprecher,C.A., Grant,F.J., Baumgartner,J.W., Presnell,S.R.,
Schrader,S.K., Yamagiwa,T., Whitmore,T.E., O'Hara,P.J. and
Foster,D.F.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-1998) Biomedical Informatics, ZymoGenetics,
Inc., 1201 Eastlake Ave. E., Seattle, WA 98102, USA
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gene
CDS
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Alignment Scores:

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AUTHORS	Baumgartner,J.W., Foster,D.C., Grant,F.J. and Sprecher,C.A.		
TITLE	Hematopoietic cytokine receptor		

JOURNAL Patent: US 5792850-A 6 11-AUG-1998;

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Location/Qualifiers

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## ORIGIN

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Job time : 7552 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	2646	4 AAS03262	Aas03262 Human cDN
2	3498	100.0	2657	10 ADD88150	Add88150 Human WSX
3	3498	100.0	2657	11 ADL26573	Adl26573 Human WSX
4	3498	100.0	2663	2 AAT94120	Aat94120 Alternati
5	3498	100.0	2663	13 ADR25231	Adr25231 Breast ca

6	3498	100.0	2677	4 AAH79286	Aah79286 Cell fact
7	3498	100.0	3258	12 ADL91800	Adl91800 Human PRO
8	3498	100.0	3258	13 ADL14162	Adl14162 Human NF-
9	3494	99.9	2628	6 ABE54548	Abes54548 cDNA enco
10	3494	99.9	2628	8 ACA61018	Acas61018 Human T-c
11	3494	99.9	2628	8 ABX10922	Abx10922 Human int
12	3490	99.8	1911	2 AACZ0863	Aacz0863 Human DNA
13	3419.5	97.8	2350	8 ACC46162	Acc46162 Human dit
14	3150	90.1	2368	2 AAT94119	Aat94119 Human hae
15	3144.5	89.9	1835	12 ADR20078	Adr20078 Human imm
16	3007	86.0	1760	2 ADO26875	Ado26875 cDNA enco
17	2875	82.2	2213	2 AAZ08867	Aaz08867 Partial h
18	2836.5	81.1	2393	10 ADB36360	Adb36360 Human imm
19	2044	58.4	2005	4 AAS03263	Aas03263 Mouse cDN
20	2044	58.4	2589	2 AAT94121	Aat94121 Mouse hae
21	886.5	25.3	1431	2 AAZ08868	Aaz08868 Partial m
22	405	11.6	817	3 AAA01659	Aaa01659 Human col
23	400	11.4	450	2 AAZ08864	Aaz08864 Mouse DNA
24	381.5	10.9	3400	12 ADK90589	Adk90589 Human IL-
25	381.5	10.9	3400	12 ADM33786	Adm33786 Human IL-
26	381.5	10.9	4040	2 AAT59731	Aat59731 Human int
27	381.5	10.9	4040	3 AAA35207	Aaa35207 Human ade
28	381.5	10.9	4040	3 AAF21329	Aaf21329 Human low
29	381.5	10.9	4040	6 ABK84394	Abk84394 Human cDN
30	381.5	10.9	4040	10 ADE39703	Ade39703 Human int
31	381.5	10.9	4040	10 ADF76394	Adf76394 Novel hum
32	381.5	10.9	4040	10 ABZ97023	Abz97023 Human nuc
33	381.5	10.9	4040	11 ABD20872	Abd20872 Human pul
34	381.5	10.9	4040	12 ADOL9579	Adol9579 Human PRO
35	381.5	10.9	4040	13 ADF54648	Adf54648 Human PRO
36	381.5	10.9	6019	3 AAA35208	Aaa35208 Human ade
37	381.5	10.9	6019	3 AAF21330	Aaf21330 Human low
38	381.5	10.9	6019	10 ABZ97024	Abz97024 Human nuc
39	381.5	10.9	6019	11 ABD20873	Abd20873 Human pul
40	331	9.5	4023	6 ABQ78355	Abq78355 Nucleotid
41	301	8.6	2546	2 AAQ11579	Aaq11579 Encodes g
42	301	8.6	2546	2 AAT47099	Aat47099 Human gra
43	301	8.6	2562	2 AAQ95481	Aaq95481 G-CSFR CD
44	299.5	8.6	2931	2 AAQ11580	Aaq11580 Clone 25-
45	299.5	8.6	2933	2 AAT47100	Aat47100 Human gra

ALIGNMENTS

RESULT 1  
AAS03262  
ID AAS03262 standard; cDNA; 2646 BP.  
XX  
AC AAS03262;  
XX  
XX  
DT 07-SEP-2001 (first entry)  
DE Human cDNA encoding type I cytokine receptor, hTCCR.  
XX

Human; type-I cytokine receptor; TCCR; T-cell differentiation; Th1; Th2;  
agonist; antagonist; autoimmune inflammatory disease;  
allograft rejection; multiple sclerosis; inflammatory bowel disease;  
insulin-dependent diabetes mellitus; infectious disease;  
human immunodeficiency virus; allergic disorder; asthma;  
allergic rhinitis; HIV; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	112..2022
FT	/*tag= a
FT	/product= "hTCCR"
FT	112..218
FT	/*tag= b
FT	219..2019
FT	/*tag= c
FT	/label= Mature_hTCCR
XX	

PN WO200129070-A2.  
 XX 26-APR-2001.  
 XX 18-OCT-2000; 2000WO-US028827.  
 PF 20-OCT-1999; 99US-0160542P.  
 XX (GETH ) GENENTECH INC.  
 XX De Sauvage FJ, Grewal I, Gurney AL;  
 PI WPI; 2001-308474/32.  
 DR P-PSDB; AAU01853.  
 XX Modulating T-cell differentiation and cytokine release profiles into Th1  
 PT and Th2 subtypes, for treating immune-related diseases in mammals, by  
 PT administering modulator of type I cytokine receptor (TCR).  
 XX Disclosure; Page 122-123; 126pp; English.  
 XX The sequence encodes human type I cytokine receptor, hTCR. The invention  
 CC relates to methods of modulating the differentiation of T-cells into the  
 CC Th2 subtype instead of the Th1 subtype, by administering a modulator of  
 CC TCR (e.g. an antagonist) to enhance, stimulate or potentiate T-cell  
 CC differentiation, or using TCR polypeptide or its agonists to prevent,  
 CC inhibit or attenuate T-cell differentiation. The mediated disease in  
 CC mammal can be created by administering a TCR antagonist and Th2 diseases  
 CC by administering a TCR agonist. Th1-mediated diseases include allograft  
 CC rejection and autoimmune inflammatory diseases, such as allergic  
 CC encephalomyelitis, multiple sclerosis, insulin-dependent diabetes  
 CC mellitus, autoimmune uveoretinitis, inflammatory bowel disease or  
 CC autoimmune thyroid disease. Th2-mediated diseases include infectious  
 CC diseases, such as leishmania major, Mycobacterium leprae, Candida  
 CC albicans, Toxoplasma gondii, respiratory syncytial virus and human  
 CC immunodeficiency virus (HIV) and allergic disorders, such as asthma,  
 CC allergic rhinitis, dermatitis and vernal conjunctivitis  
 XX Sequence 2646 BP; 566 A; 779 C; 789 G; 511 T; 0 U; 1 Other;

Alignment Scores:  
 Pred. No.: 1.8e-164 Length: 2646  
 Score: 3498.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-088-950A-1 (1-636) x AAS03262 (1-2646)

QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
 DB 112 ATGCGGGAGGAGGCGGCGCCCTTTCTGGCTGTGGCGCGCTGCCAAGCTGGCGTGTG 171

QY 21 ProLeuLeuTrpValLeuPheGlnAArgTrpArgProGlnGlySerAlaGlyProLeuGln 40  
 DB 172 CCTCTGTGTGGGTGTCTTTCAGCGGAGCGGTCCCGAGGAGCGCGCGGCGCATGCGAG 231

QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60  
 DB 232 TGCTACGGAGTTGGACCCCTTGGCGGACTTGAACCTGCTCGTGGGAGCTCTTGGGACCTG 291

QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
 DB 292 GGAGCCCCCTCCAGGTACACCTCCAGAGCCAAAGTACCGTTCACCAACAAACCCAGACT 351

QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
 DB 352 GTGGCAGTGGCAGCGGACCGGAGCTGGTGGCCATTCTCTGGGAAACAGCTCACCATGCT 411

QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
 DB 412 GACAAACTCCTTGTCTGGGGGCACTAAGGGGAGGCGGAGCCCTCTCTGGCGCCCGCTTCTG 471

QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 DB 472 AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGGCTGGGCGCTGAGCGTGTTCCTCC 531

QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
 DB 532 GAGGATGACCCCTGGAGGCGCACTGTCCATTGGGCGCCACCTACATGGCCATCTCATAA 591

QY 161 ValLeuLysCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
 DB 592 GTTCTGATCTGCCAGTCTCCACTACCGAAGATGTACGAGGCGGCGCTGGACCCCTGTG 651

QY 181 ProGluLeuLysThrIleProLeuThrProValGluLysGlnAspLeuGluLeuAlaThr 200  
 DB 652 CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTGGAGTACCCACT 711

QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220  
 DB 712 GGTACAAAGTGTATGGCGCTGCGGATGGAGAAAGAGGATTTGTGGGCGGAGTGG 771

QY 221 SerProLysLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
 DB 772 AGCCCCATTTTGTCTTCAGACACCCGCTTCTGCTCCAAAGATGTGTGGGTATCAGGG 831

QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
 DB 832 AACCTCTGTGGAGCCCTGGAGGAGGAGACCTTGTCTTATGGAAAGCCCGGCGCC 891

QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
 DB 892 TGTGTGAGGTGAGCTACAAAGTCTGGTCTGGGTTCGAGTCTGTGAGTCCAGAA 951

QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
 DB 952 GGAATTACTGTGTGTCTGCTCCCTTAATCCAGTGGGCGGAGTGGGCGGAGTGTCCGCT 1011

QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
 DB 1012 GTCAACGCCACAGCTGGAGGCTCTCAACCACTCTCTTGTGTGTGTGGTTCAGGCC 1071

QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
 DB 1072 TCTGCCCCCGGTAGCGTGGCAGTACAGCAGTCTGGGAGCGCAGCAGTACTGTGTACC 1131

QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
 DB 1132 TGGCAACCGGGCGCTGGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGTGGGAC 1191

QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
 DB 1192 CCCCCTGGAGAAACTCAACTCAGGTCCGGCTTCCCCCTGGGAACCTCAGTGTCTGTACCA 1251

QY 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
 DB 1252 GGGAAATTCACCTGTCCGGGTCCCTTATCGAATCACTGTGACCGCAGTCTCTGTTCAGC 1311

QY 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
 DB 1312 TTGGCTCTCGCATCTCCGTCTGGGGGTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA 1371

QY 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
 DB 1372 AGCTTTTGGGACTCAAGATGCCCTCTCAGGGACCCCGCCCATAGCTGGGGAGAGTTC 1431

QY 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460  
 DB 1432 CCAAGGCGCAGCTCGAGGCGCCCTCACCCTACACTACCTTGTGTGCACAGAGTGGAAAC 1491

QY 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
 DB 1492 AGCCCCCTCGTGTGATGAATGTGAGTGGCAACACACAGAGGTGTCAACCTGCTGACCTT 1551



481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
 1552 CTTGGGGTCCCTGTGAGCTGTGGGTGACGATCTACCATCGCTGGACAGGGCCCTCT 1611  
 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
 1612 GGTCCCATCTCCGGCTTCATCTACCAAGATACACCTGAGTGGAAAGTTCTGCCGGC 1671  
 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
 1672 ATCCTATTCTGTGGGGTGTTCCTGTGTGGGGTGTGGCCTGAGCCTGGCCACCTCTGGA 1731  
 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
 1732 AGGTGCTACCACTTAAGGCACAAAGTGTGCCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1791  
 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
 1792 CTGCCCACAGCAGTTTCAGGCCAGCCCAACATGAGGACAGTACCTGAGGCCAGCCCTT 1851  
 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600  
 1852 GGGGACTTGGCCATCTCTGGAAGTGGAGAGATGAGAGCCCGCGGTTATGGAGTCTCC 1911  
 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
 1912 CAGCCGCCAGGACCGCCCGCTTGTGACTCTGGGTATGAGAGACATCTCTGCCACACA 1971  
 621 ProGluGluLeuGlyLeuGlyProProArgProGlnValLeuAla 636  
 1972 CTGAGGAGCTGGGCTTCTGGGGCCCCCGCCAGGCCACAGGTCTTGGCC 2019  
 RESULT 2  
 ADD68150  
 ID ADD68150 standard; cdna; 2657 BP.  
 AC ADD68150;  
 XX  
 DT 15-JAN-2004 (first entry)  
 DE Human WSX-1 receptor cDNA SEQ ID NO:8.  
 XX  
 KW ss; gene; human; zcytor17; antiinflammatory; dermatological;  
 KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;  
 KW toxic shock syndrome; infectious disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 133..2043  
 FT /\*tag= a  
 FT /product= "WSX-1 receptor"  
 XX  
 PN WO200306090-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PF 21-JAN-2003; 2003WO-US001984.  
 XX  
 PR 18-JAN-2002; 2002US-0350325P.  
 PR 25-APR-2002; 2002US-0375323P.  
 PR 19-DEC-2002; 2002US-0435315P.  
 PR  
 PA (Zymo) ZYMOGENETICS INC.  
 XX  
 PI Sprecher CA, Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;  
 PI Novak JE, Gross JA, Dillon SR;  
 XX  
 DR WPI; 2003-618179/58.  
 DR P-PSDB; ADD68151.  
 XX

PT New zcytor17 ligand polypeptides, useful for treating inflammatory  
 PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's  
 PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.  
 XX  
 PS Example 3; SEQ ID NO 8; 372pp; English.  
 XX  
 CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A  
 CC polypeptide of the invention has antiinflammatory, dermatological,  
 CC immunosuppressive, and antimicrobial activity, and may have a use in a  
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,  
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
 CC shock syndrome or infectious diseases. The present sequence is used in  
 CC the exemplification of the invention.  
 XX  
 SQ Sequence 2657 BP; 556 A; 789 C; 800 G; 512 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.8e-164 Length: 2657  
 Score: 3498.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0  
 US-10-088-950A-1 (1-636) x ADD68150 (1-2657)  
 QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
 DB 133 ATCGGGGAGGAGGGGGCCCTTCTGTGGCTGTGGCCGCTGCCAAGCTGGGCTGCTG 192  
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
 DB 193 CCTCTGTGTGGGTGCTTTTCCAGCGACGCGTCCCAGGCGAGCGCGGCCACTGCAG 252  
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60  
 DB 253 TGTACGGAGTTGGACCCCTTGGGCGACTTGAACCTGCTCGGGAGCGCTCTTGGGAGCTG 312  
 QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
 DB 313 GGAGCCCCCTCCAGTTTACACTCCAGAGCCAAAGTACCTTCCACAAACCCAGACT 372  
 QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
 DB 373 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGCT 432  
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
 DB 433 GACAAACTCCTTCTGTGGGCGACTAAGGCGAGCGCGCTCTCTGGCCCCCGCTTCTG 492  
 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 DB 493 AACCTAGAAACCCCAATGAAGCCAAACGCCCGCTGGGCGCTGACGTGGACTTTTCC 552  
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
 DB 553 GAGGATGACCCCTCGGAGGCGCACTGTCCATTGGGCCCCACCTACATGSCCATCTCATAA 612  
 QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
 DB 613 GTTCTGATCTGCCAGTTTCCACTACCGAAGATGTGAGGAGCGGCGCTGGACCTGCTGAA 672  
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
 DB 673 CCGAGCTGAAGACCATACCCCTGACCCCTTTGAGATCCAAAGATTGGAGCTAGCCACT 732  
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220  
 DB 733 GGCTACAAAGTGTATGGCCGCTGCCGATGAGAGAAAGAGAGATTTGTGGGCGAGTGG 792  
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240

793 AGCCCATTTTGTCTTCCAGACACCGCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 852  
 241 AsnLeuGlyThrProGlyGlyGluProLeuLeuLeuTrpValProGlyPro 260  
 853 AACCTCTGTGGAGCGCTCGAGAGAGAACCTTTGCTTCTATGGAAGGCCCCAGGGCCC 912  
 261 CysValGlnValSerTrpValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
 913 TGTGTGAGGTGAGCTACAAAGTGTGTTGGTTGGAGGTCTGAGTCCAGAA 972  
 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
 973 GGAATTTACCTGTCTGCTCCCTTAATTCAGTGGGGCGAGTGGGCCAGGGTCTCCGCT 1032  
 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
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 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
 1093 TCTGCCCCCGTAGCTGGCAGTCAGCAGCATCGCTGGGAGCAGGAGTACTGTGACC 1152  
 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
 1153 TGGCAACCGGGGCTTGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1212  
 361 ProLeuGluValAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuPro 380  
 1213 CCCCTGGAGAACTCAACTGGGTGGGCTTCCCTGGGAACCTAGTGTCTCTGTATACA 1272  
 381 GlyAsnPheThrValGlyValProTrpArgIleThrValThrAlaValSerAlaSerGly 400  
 1273 GGGATTTTCACTGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGC 1332  
 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
 1333 TTGGCCTCTGCATCTCCCTCTGGGGGTTTGGGAGGAATAGCACCCCTAGTGGGGCA 1392  
 421 ThrLeuTrpArgLeuGlnAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
 1393 AGCTTTTGGGAGCTCAAGATGCCCTCTCAGGAGCCCGCCATAGCTGGGGAGAGTTC 1452  
 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTrpLeuCysAlaGlnSerGlyThr 460  
 1453 CCAGGCACCACTTGGAGCCACCTCACCCACTACACCTTGTGTGCAGAGTGGAACT 1512  
 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
 1513 AGCCCTCTCCGCTGTGATGAATGTGAGTGGCAACACACAGAGTGTCACTGCTGACCTT 1572  
 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
 1573 CTTTGGGGTCTCTGTGAGTGTGGGTGAGCAGCATCTACCATCGCTGGAGAGGCTCTCT 1632  
 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpIleValLeuProGly 520  
 1633 GTTCCCATCTCTCGGCTTCTATCCAGATACACCTCGAGTGGAGAAATCTTGGCAGC 1692  
 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
 1693 ATCTATTCTTGTGGGGCTTGTCTGTGGGGTGTGGCTGAGCTGGCCACCTCTGGA 1752  
 541 ArgCysTrpHisLeuArgHisValLeuProArgTrpValTrpGluValValProAsp 560  
 1753 AGGTGCTACCACTAAGGCACAAAGTGTGCCCGCTGGGTCTGGAGAAAGTCTCTGAT 1812  
 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
 1813 CTGTCCACAGCAGTTCAGCCAGCCACATGGAGCAAGTACTTGGAGCCCGAGCCCTT 1872  
 581 GlyAspLeuProIleLeuGluValGluMetGluProProValMetGluSerSer 600  
 1873 GGGGACTTGCCTATCTGGAAGTGGAGAGATGGAGCCCGCCGCTTATGAGTCTCTCC 1932

QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTrpGluValHisPheLeuProThr 620  
 Db 1933 CAGCCCGCCAGCCAGCCAGCCCGCTTGACTCTGGTATGAGAGACATCTTCTGCCACA 1992  
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
 Db 1993 CCTGAGGAGCTGGGCTTCTTGGGGCCCCCAGCCACAGGTTCTGGCC 2040  
 RESULT 3  
 ADL26573  
 ID ADL26573 standard; DNA; 2657 BP.  
 XX  
 AC ADL26573;  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human WSX-1 receptor DNA.  
 KW antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;  
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;  
 KW immune response inhibitor; inflammatory response inhibitor;  
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;  
 KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;  
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;  
 KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;  
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;  
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;  
 KW septicemia; toxic shock syndrome; zcytor17lig; human; gene; ds;  
 KW zcytor17 ligand; WSX-1 receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003215838-A1.  
 XX  
 PD 20-NOV-2003.  
 XX  
 PF 21-JAN-2003; 2003US-00351157.  
 XX  
 PR 18-JAN-2002; 2002US-0350325P.  
 PR 14-JUN-2002; 2002US-0389108P.  
 PR 19-DEC-2002; 2002US-0435361P.  
 XX  
 PA (SPRE/) SPRECHER C A.  
 PA (GAOZ/) GAO Z.  
 PA (KUIJ/) KUIJPER J L.  
 PA (DASO/) DASOVICH M M.  
 PA (GRAN/) GRANT F J.  
 PA (PRES/) PRESNELL S R.  
 PA (WHIT/) WHITMORE T E.  
 PA (HAMM/) HAMMOND A K.  
 PA (NOVA/) NOVAK J E.  
 PA (GROS/) GROSS J A.  
 PA (DILL/) DILLON S R.  
 XX  
 PI Sprecher CA, Gao Z, Kuijper J L, Dasovich MM, Grant FJ;  
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;  
 XX  
 DR WPI; 2003-876545/81.  
 DR P-PSDB; ADL26574.  
 XX  
 PT Novel multimeric or heterodimeric cytokine receptors useful for treating  
 PT chronic inflammatory disease such as inflammatory bowel disease,  
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,  
 PT septicemia.  
 XX  
 PS Example 3; SEQ ID NO 8; 205pp; English.  
 XX  
 CC The invention describes an isolated multimeric or heterodimeric cytokine  
 CC receptor (I) having at least one polypeptide having 90 percent sequence  
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in  
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino  
 CC acid sequence, given in specification, or at least one polypeptide

comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (C1) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor17lig-induced proliferation or differentiation of hematopoietic cells and hematopoietic progenitor cells; reducing zcytor17lig-induced inflammation; treating a mammal afflicted with an inflammatory disease in which zcytor17lig plays a role. The disease is a chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and psoriasis. The disease is acute inflammatory disease such as endotoxaemia, septicemia, toxic shock syndrome and infectious disease. An immune response inhibiting composition is useful for inhibiting an immune response in a mammal exposed to an antigen or pathogen. An inflammatory response inhibiting composition is useful for suppressing an inflammatory response in a mammal with inflammation. An antibody that specifically binds to (I) is useful for detecting the presence of a multimeric or heterodimeric cytokine receptor in a biological sample. CC This sequence encodes a human WSX-1 receptor used in the creation of a CC vector expressing full length zcytor17.

XX Sequence 2657 BP; 556 A; 789 C; 800 G; 512 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	1.8e-164	Length:	2657
Score:	3498.00	Matches:	636
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-088-950A-1 (1-636) x ADL26573 (1-2657)

Qy	1	MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	133	ATGGGGGAGGCGAGGGGGCCCCCTTTCTGGGTGGGGCGCTGGCCCAAGCTGGGGCGCTCTG	192
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	193	CCCTCTGTGTGGGTCTTTCCAGCGGACGGCTCCCGAGGGCAGCGCGGGCCACTGCAG	252
Qy	41	CysTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	253	TGCTACGGAGTTGACCCCTTGGGCGACTTGAACCTGCTCGTGGGAGCCCTCTGGGGACCTG	312
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTrpArgSerAsnLysThrGlnThr	80
Db	313	GGAGCCCCCTCCGAGTTACACCTCCAGAGGCCAAAGTACCCTTTCCAAACAAACCCAGACT	372
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	373	GTGGCAGTGGCAGCGGAGCGAGCTGGGTGGCCATTCTCTGGGAACAGCTCACCATGTCT	432
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal	120
Db	433	GACAAATCTCTGTCTGGGCACTAAGCGAGGCGAGCCCTCTCTGGCCCCCGCTTCTGTG	492
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	493	AACTAGAAACCCCAATGAAAGCCAAACGCCCGCGGTGGGCGCTGACGTGGACATTTTTC	552
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	553	GAGGATGACCCCTGGAGGGCACTGTCCATTTGGGCCCCACCTACATGGCCATCTCATAAA	612
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaIleTrpThrLeuLeuGlu	180
Db	613	GTTCGTGATCTGCCAGTCTCCACTACCGAAGATGTCCAGGAGGGCGGCTGACCCCTGTGAA	672
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	673	CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTTGGAGCTAGCCACT	732

Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp	220
Db	733	GGCTACAAAGTGTATGGCCCTGCCGATGGAGAAAGAGAGGATTTGTGGGGCGAGTGG	792
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	793	AGCCCCATTTTGTCTTCCAGACACCGCCCTTCTGCTCCAAAGATGTGTGGGTATCAGGG	852
Qy	241	AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	853	AACTCTGTGGGAGCGCTGGAGAGAGAACTTTGTCTTATGGAAAGGCCCCAGGGGCC	912
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGlyLeuSerProGlu	280
Db	913	TGTGTGCAGGTGAGCTACAAAGTCTGGTTCTGGGTGGAGTCTGTGAGTCCAGAA	972
Qy	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
Db	973	GGAAATTACCTGTGCTGCTCCCTAAATTCAGTGGGGCGAGTGGGGCGAGGTCTCGCT	1032
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	1033	GTCAACGCCCAAGCTGGAGCCCTCTCACCAACCTCTCTTTGGTCTCTTGATTCAGCC	1092
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
Db	1093	TCTGCCCCCGTAGCTGGCGAGTCAGAGCATCGCTGGGAGCAGGAGCTACTGTGTACC	1152
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
Db	1153	TGGCAACCGGGGCTCGGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC	1212
Qy	361	ProLeuGluLysLeuLeuTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
Db	1213	CCCTTGAGAAATCTCAACTGGGTCCCGCTTCCCGCTGGGAACCTCAGTGTCTGTATACA	1272
Qy	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
Db	1273	GGGAATTTCACTGTGGGGTCCCTTCATCGAATCACTGTACCGCAGCTCTCTGTTCAGGC	1332
Qy	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluLeuAlaProLeuValGlyPro	420
Db	1333	TTGGCCTCTGCATCTCCGCTCTGGGGGTTTCCAGGAGGAATAGCACCCCTAGTGGGGCCA	1392
Qy	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
Db	1393	ACGCTTTGGCGACTCCAAAGATGCCCTTCAGGGAGCCCCCGCCATAGCGTGGGAGAGGTC	1452
Qy	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
Db	1453	CCAGGCACACAGCTTCAGGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGGAAACC	1512
Qy	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
Db	1513	AGCCCCCTCCGTCTGCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT	1572
Qy	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
Db	1573	CCTTGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCCT	1632
Qy	501	GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly	520
Db	1633	GGTCCCATCTCCGGCTTCATCTACAGATACACCTCAGGTGGAAAGTCTCTGCCAGGC	1692
Qy	521	IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
Db	1693	ATCCTATTCTTGGGGCTTGTCTCTCTGGGTGTGGCTGAGCTGAGCTGGCCACCTCTGGA	1752
Qy	541	ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp	560
Db	1753	AGGTGCTACCACTAAGGCAAAAGTGTGCCCCCTGGGTCTGGGAGAAAGTTCCTGAT	1812

QY 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
 Db 1813 CTGCGCAACAGCAGTTTCAGCCAGCCACATGAGCAAGTACCTGAGGCCAGCCCTT 1872  
 QY 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600  
 Db 1873 GGGGACTTCCCATCTCGAAGTGGAGGAGATGGAGCCCGCCCGTTATGAGTCTCC 1932  
 QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluGluHisPheLeuProThr 620  
 Db 1933 CAGCCCGCCAGCCACCCCGCTTGACTCTGGGTATGAGAGCATTCTGCGCCACA 1992  
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
 Db 1993 CCTGAGGAGCTGGCCCTCTCGGGGCCCCCGCCAGCCACAGCTTCTGGCC 2040  
 RESULT 4  
 AAT94120  
 ID AAT94120 standard; cDNA; 2663 BP.  
 AC AAT94120;  
 XX 22-MAY-1998 (first entry)  
 DE Alternatively spliced Zcytor1 cDNA.  
 XX Human: haematopoietic cytokine receptor; Zcytor1; ligand detection;  
 KW cancer diagnosis; agonist; antagonist; alternatively spliced; ds.  
 XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 139..2049  
 FT /\*tag= a  
 FT /product= "Zcytor1"  
 PN WO9744455-A1.  
 XX 27-NOV-1997.  
 PD 19-MAY-1997; 97WO-US008502.  
 XX 23-MAY-1996; 96US-00653740.  
 PR (ZYMO ) ZYMOGENETICS INC.  
 PA Baugartner JW, Foster DC, Grant FJ, Sprecher CA;  
 XX WPI; 1998-018509/02.  
 DR P-PSDB; AAW33399.  
 XX Haematopoietic cytokine receptor - useful for ligand detection, and  
 PT pathological condition diagnosis.  
 XX Claim 13; Page 46-51; 86pp; English.  
 CC The present sequence encodes an alternatively spliced human  
 CC haematopoietic cytokine receptor Zcytor1, useful for ligand detection,  
 CC and pathological condition diagnosis, including cancer. Receptor agonists  
 CC of the protein can be used to stimulate the proliferation and development  
 CC of target cells in vitro and in vivo. The agonists can stimulate cell  
 CC mediated immunity and lymphocyte proliferation, to treat infection  
 CC involving immunosuppression, e.g. viral infections. They may also be used  
 CC to suppress tumours, induce cytotoxicity, treat leukopenias and enhance  
 CC the regeneration of the T-cell repertoire after bone marrow  
 CC transplantation. Antagonists of the protein may be used to suppress the  
 CC immune system, treat autoimmune diseases, including rheumatoid arthritis,  
 CC multiple sclerosis and diabetes mellitus. Immune suppression caused by  
 CC the antagonists can also be used to reduce rejection of tissue or organ  
 CC transplants and grafts, and to treat T-cell specific leukaemias and  
 CC lymphomas  
 XX Sequence 2663 BP; 558 A; 790 C; 803 G; 512 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,81e-164 Length: 2663  
 Score: 3498.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-088-950A-1 (1-636) x AAT94120 (1-2663)  
 QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
 Db 139 ATCGGGGAGGAGGGGGCGCCCTTTCTGCTGTGTGGCGCTGCCCAAGTGGCGTGTG 198  
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
 Db 199 CCTCTGTGTGGTGTCTTTCCAGCGGACGGCTCCAGGCGAGCGCGGGCCACTGAG 258  
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysserTrpGluProLeuGlyAspLeu 60  
 Db 259 TGCTACGGAGTTGGACCTTGGCGGACTTGAAGTCTGTGGAGGCTCTTTGGGACCTG 318  
 QY 61 GlyAlaProSerGluLeuHisGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
 Db 319 GGAGCGCCCTCCGAGTTACACTCCAGAGCCCAAAAGTACCGTTCCCAACAAACCCAGACT 378  
 QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
 Db 379 GTGGCAGTGGCAGCGGACGGAGCTGGGTGGCCATTCTCGGAAACAGCTACCATGCT 438  
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
 Db 439 GACAACTCCCTGTCTGGGGCCTTAAGGCAGGCCAGCTCTCTGGCCCCCTCTTCGTG 498  
 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 Db 499 AACCTAGAAACCCAAATGAAGCCAAACGCCCGCGCTGGGGCCTGAGCTGGACTTTTCC 558  
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
 Db 559 GAGGATGACCCCTCTGGAGGCCACTGTCTATTGGGGCCCCACCTACATGGCCATCTCATATA 618  
 QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
 Db 619 GTTCTGATCTGCAGTTCACCTACCGAAGATGTCAGGAGGGCGCTGGACCTGTGGAA 678  
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluAlaThr 200  
 Db 679 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAAGATTTGAGTAGCCACT 738  
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220  
 Db 739 GGCTACAAAGTGTATGGCCGCTGCGGATGGAGAAGAAGAGGATTTGGGGCGGAGTGG 798  
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
 Db 799 AGCCCCATTGTCTCTTCAGACACCGCTTCTGTCTCCAAAGAGATGTGGGTATCAGGG 858  
 QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
 Db 859 AACCTCTGTGGGACCCCTGGAGGAGGAACCTTTGTCTTATGGAAGCCCGGCGGCC 918  
 QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
 Db 919 TGTGTGAGGTGAGTACAAAGTCTGGGTGGAGGTCTGGTGGAGTCTGAGTCTGAGTCCAGAA 978  
 QY 281 GlyIleThrCysCysSerSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
 Db 979 GGAATTACTGTCTGTCTCCCTAATTCAGTGGGGCGGAGTGGGCCAGGGGTGTCCGCT 1038  
 QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320

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Db 1039 GTCACGCCCAAGCTGGAGCCCTCTCACCACCTCTCTTGGTCTGCTGGATTCAGCC 1098
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
Db 1099 TCTGCCCCCGTAGCGTGGCAGTTCAGCAGCATCGCTGGAGCAGGAGCTACTGGTACC 1158
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1159 TGGCAACCGGGGCTGGGGAACCACTGGAGCATGTAGTGGAGCTGGGCTCGAGATGGGAC 1218
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyValAsnLeuSerAlaLeuPro 380
Db 1219 CCCCTGGAGAACTCAACTGGTGGGCTTCCCTCGGAACTTCAGTCTCTGTATACCA 1278
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1279 GGGAAATTTCATGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1338
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1339 TTGGCCCTCTGCATCTCGCTTGGGGTTCAGGAGGAATTAGCACCCCTAGTGGGGCCA 1398
Qy 421 ThrLeuTrpArgLeuGlnAsnAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1399 ACGTTTGGGACATCCCAAGATGCCCTCCAGGGACCCCGCATAGCGTGGGAGAGGTC 1458
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1459 CCAAGGACACAGCTTCAGGCCACCTCACCACCTACCTTGTGTGCACAGATGGNACC 1518
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1519 AGCCCTCTCGCTGCGATGATGTAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1578
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1579 CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGTGGACAGGGCCCTCCT 1638
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1639 GGTCCCATCTCCGGCTTCATCTACCAAGTAACACCTCTGAGGTGGAAAGTTCTGCCAGGC 1698
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1699 ATCTATTCTTGTGGGCTTGTTCCTGTGGGGTGTGGCTGAGCCTGGCCACCTCTGGA 1758
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1759 AGGTGCTACCATCTAAGGCCAAGATGCTGCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT 1818
Qy 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1819 CTGTGCCAACAGAGTTTCAGGCCAGCCCCACCATGAGCAAGTACTCTGAGGCCCCAGCCCTT 1878
Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600
Db 1879 GGGGACTTGCCTCTCTGGAAGTGGAGAGATGAGAGCCCCCGCGGTATATGGAGTCTCTCC 1938
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1939 CAGCCGCCAGGCGCACCGCCCGCTTGACTCTGGGTATGAGAAGCAGCTTCTCTGCCACA 1998
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1999 CCTGAGGAGCTGGGCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTTGCC 2046
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## RESULT 5

ADR25231

ID ADR25231 standard; DNA; 2663 BP.

XX

AC ADR25231;

XX

DT 21-OCT-2004 (first entry)

XX Breast cancer prognosis marker #1092.

DE ds; breast cancer; prognosis; gene expression; diagnosis.

KW Homo sapiens.

OS WO2004065545-A2.

PN 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.

XX 15-JAN-2003; 2003US-00342887.

XX (ROSE-) ROSETTA INPHARMATICS LLC.

PA (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

PI WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.

PS Disclosure; SEQ ID NO 1092; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.

SQ Sequence 2663 BP; 558 A; 790 C; 803 G; 512 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	1.81e-164	Length:	2663
Score:	3498.00	Matches:	636
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-088-950A-1 (1-636) x ADR25231 (1-2663)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20

Db 139 ATCGGGGAGGAGGAGGGGCGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGGGCTGCTG 198

Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

Db 199 CCTCTGTGTGGTGTCTTTTCCAGCGGACGCGTCCCCAGGGCAGCGCGGGCCACTGCAG 258

Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 259 TGCTACGGAGTTGGACCCCTTGGCGACTTGAACTGCTGTGGGAGCGCTCTTGGGAGCTG 318

Qy 61 GlyAlaProSerGluLeuHisIleuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80

Db 319 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCCAACAAACCCAGACT 378

Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100

Db 379 GTGGCAGTGGCAGCCCGAGCGAGCTGGTGGCCATTCTTCGGGAACAGCTCACCATGTCT 438

Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120

Db 439 GACAAACTCCTTGTCTGGGGCACTAAGGAGGAGGCGAGCCTCTCTGGGCCCCCGCTTCTGGTG 498  
 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 Db 499 AACCTAGAAACCAATGAAGCAACACGGCCCCCGGCTGGGCGCTGACGTGGACTTTTCC 558  
 QY 141 GluAspAspProLeuGluAlaThrValHisTyrAlaProProThrTyrProSerHisLys 160  
 Db 559 GAGGATGACCCCTGGAGGCACTGTCATTTGGGCCCCACCTACATGGCCATCTCATAAA 618  
 QY 161 ValLeuLeuCysGlnPheHisTyrArgArgCysGlnGluAlaAlaThrThrLeuLeuGlu 180  
 Db 619 GTTCTCATCTGCCAGTTCCACTACCGAAGATGTCAGAGGCGGCTGGACCTGCTGGAA 678  
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluAlaThr 200  
 Db 679 CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTGGAGCTAGCCACT 738  
 QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluLysLeuLeuThrProGlyLys 220  
 Db 739 GGCTACAAAGTGTATGGCCGCTGCCGATGGAGAAAGAGATTGTGGGGCGAGTGG 798  
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTyrValSerGly 240  
 Db 799 AGCCCCATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 858  
 QY 241 AsnLeuCysGlyThrProGlyGlyGluLysProLeuLeuLeuThrLysAlaProGlyPro 260  
 Db 859 AACCTCTGTGGAGCGCTGGAGAGAGAACCTTTGCTTCTATGGAAGGCCCCAGGGGCC 918  
 QY 261 CysValGlnValSerTyrLysValTyrPheTyrValGlyArgGluLeuSerProGlu 280  
 Db 919 TGTGTCCAGTGAGCTACAAAGTCTGTGTTGGTTGGAGGTCGTGAGTGCAGTCCAGAA 978  
 QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluThrAlaArgValSerAla 300  
 Db 979 GGAATTTACCTGCTGCTGCTCCCTTAATCCAGTGGGGCGAGTGGGCCAGGGTGTCCGCT 1038  
 QY 301 ValAsnAlaThrSerTyrGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
 Db 1039 GTCAACGCCACAAGCTGGGAGCGCTCTCACCAACCTCTCTTGGTCTGCTTGGATTGAGCC 1098  
 QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
 Db 1099 TCTGCCCCCGTAGCTGGAGTGCAGTGCAGCATGCTGGAGACGAGGACTACTGTGACC 1158  
 QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
 Db 1159 TGGCAACCGGGGCTGGGGAACCCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1218  
 QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
 Db 1219 CCCCTGGAGAACTCAACTAGGTCGGGTCGGGCTTCCGCCCTGGGAACCTCAGTGTCTGTATACCA 1278  
 QY 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
 Db 1279 GGGAAATTTCACTGTGGGGTCCCTATCGAATCACTGTGACCGAGCTCTGCTTCAGCG 1338  
 QY 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
 Db 1339 TTGGCTCTGCATCTCCCTGCTGGGGGTTTCAGGAGGAATTAGCACCCCTAGTGGGGCCA 1398  
 QY 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaThrProGlyGluVal 440  
 Db 1399 AGCTTTGGCGACTCCAAGATGCCCTCCAGGAGACCCCGCCATAGCGTGGGGAGAGTTC 1458  
 QY 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460  
 Db 1459 CNAAGGACACAGCTTCAGGCGCCACTCACCCACTACCTTGTGTGCCAGAGTGGAAAC 1518  
 QY 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
 Db 1519 AGCCCCCTCGCTGTGCATGAATGTAGTGGCAACACACAGAGTGTCAACCCTGCTGACCTT 1578

QY 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
 Db 1579 CTTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1638  
 QY 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
 Db 1639 GGTCCCATCTCCGCTTCATCTACAGATAACACCTGAGGTGGAAAGTTCTGCCAGGC 1698  
 QY 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
 Db 1699 ATCTTATTTCTGTGGGGCTGTCTTCTGTGGGGTGTGGCTGAGCCTGCGCACCTCTGGA 1758  
 QY 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
 Db 1759 AGGTCTCTACCACTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT 1818  
 QY 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
 Db 1819 CTTGCCACACAGCAGTTCAAGGCCAGCCCCACATGGAGCAAGTACCTGAGGCCAGCCCTT 1878  
 QY 581 GlyAspLeuProIleLeuGluValGluMetGluProProProProValMetGluSerSer 600  
 Db 1879 GGGGACTTGGCCCATCTCGAAAGTGGAGGAGATGGAGCCCGCCCGCTTATGGAGTCTCC 1938  
 QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
 Db 1939 CAGCCCGGCCAGGCCACCGCCCGCTTACTTGGGTATGAGAACACTTCTCTGCCACA 1998  
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
 Db 1999 CTTGAGGAGCTGGGCTTCTGGGGCCCCCGCCAGGCCACAGGTCTCTGGCC 2046

## RESULT 6

AAH79286  
 ID AAH79286 standard; cDNA; 2677 BP.  
 XX  
 AC AAH79286;  
 XX  
 DT 20-NOV-2001 (first entry)  
 XX  
 DE Cell factor receptor CRL1 coding sequence.  
 XX  
 KW Cell factor receptor; CRL1; gpl30; cancer; inflammation;  
 KW immunological rejection; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN CN1299828-A.  
 XX  
 PD 20-JUN-2001.  
 XX  
 PF 16-DEC-1999; 99CN-00124269.  
 XX  
 PR 16-DEC-1999; 99CN-00124269.  
 XX  
 PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.  
 XX  
 PI Cao X, Zhang W, He L;  
 XX  
 DR WPI; 2001-523189/58.  
 DR P-PSDB; AAG65270.  
 XX  
 PT New cell factor acceptor, its code sequence and use.  
 XX  
 PS Claim 5; Page 17-18; 27pp; Chinese.  
 XX  
 CC The present invention provides the protein and coding sequences of a  
 CC novel cell factor receptor, designated CRL1. This is a homogeneous  
 CC molecule of gpl30. The sequences can be used in the treatment of cancer,  
 CC inflammation and immunological rejection. The present sequence is the  
 CC coding sequence of the invention



SQ Sequence 2677 BP; 581 A; 786 C; 798 G; 512 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.82e-164 Length: 2677  
Score: 3498.00 Matches: 636  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

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Qy	1	MetArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	126	ATGCGGGAGGACGGGGCGCCCTTCTGGCTGTGGCGCTGCCCAAGCTGGCGTCTG	185
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
Db	186	CCTCTGTGTGGGTGCTTTTCCAGCGGACGGCTCCCGAGGGCAGCGCGGGCCACTGCAG	245
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	246	TGCTACGGAGTGGACCTTGGGCGACTTGNACTGCTGTGGGAGCCCTCTTGGGACCTG	305
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	306	GGAGCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	365
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	366	GTGCACTGGCGAGCGGACGGAGCTGGGTGGCCATTCTCTGGGAAACAGCTCACCATGCT	425
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
Db	426	GACAACTCCTTGTCTGGGGCATTAAGCGAGCGCCAGCTCTCTGGCCCCCGCTTCTGTG	485
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	486	AACCTAGAAACCCAAATGAAGCCAAACGCCCGCGCTGGGCCCTGACGTGGACTTTTTC	545
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	546	GAGGATACCCCTCGGAGGCACTGTCTATTTGGGCCCCACCTACATGGCCATCTCTATAA	605
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
Db	606	GTCTGTATCTGCCAGTCTCCACTACCGAAGATGTCCAGAGGGCGCTGGACCTGCTGGAA	665
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	666	CCGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTGGAGCTAGCCACT	725
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
Db	726	GGCTACAAAGTGTATGCCCGCTGCGGATGAGAAAGAGGATTTGTGGGGCGAGTGG	785
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	786	AGCCCCATTTGTCTTCCAGACACCCGCTCTGCTCCAAAGATGTGGGTATACAGG	845
Qy	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	846	AACCTCTGTGGAGCCCTGGAGGAGAGAACCTTTGCTTATGGAGGCCCCAGGGCCC	905
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	906	TGTGTGAGGTGAGTACAAAGTCTGGTTCTGGGTTGGAGTCTGTAGCTGAGTCCAGAA	965
Qy	281	GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
Db	966	GGAAATACCTGCTGCTCTCCCTAAATCCAGTGGGGCGGAGTGGGGCGAGGTCCGCT	1025
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320

RESULT 7

ADL91800

ID ADL91800 standard; cDNA; 3258 BP.

XX

AC ADL91800;

XX

Db	1026	GTCAAGCCACAAAGCTGGGAGCCTCTCAACAACCTCTCTTTGGTCTCTCTGGATTACGCC	1085
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
Db	1086	TCGCCCCCGGTAGCGTGGGAGTACAGAGCATCGCTGGGAGCACGGAGCTACTGGTACCC	1145
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
Db	1146	TGGCAACCGGGGCTGGGAAACCACTGGAGCATGTAGTGAGCTGGGCTCGAGATGGGAC	1205
Qy	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
Db	1206	CCCTTGAGAGAACTCAACTGGGTCCGCTCCGCTGGGAACTTACAGCTCTCTGTACCA	1265
Qy	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
Db	1266	GGGAATTTCACTGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGTCTCAGGC	1325
Qy	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
Db	1326	TTGGCCTCTGCATCTCCGCTCGGGGTTTCAGGGAGGAATTAGCACCCCTAGTGGGCCA	1385
Qy	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
Db	1386	ACGCTTTGGCGACTCCCAAGATGCCCTCCAGGGACCCCGCCCATAGCGTGGGAGAGGTC	1445
Qy	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
Db	1446	CCAAGGACCAAGCTTCAGGCGCCACCTACCCACTTGTGTGCACAGAGTGGAAACC	1505
Qy	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
Db	1506	AGCCCTCTCGTCTGCATGATGTAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT	1565
Qy	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
Db	1566	CCTTGGGTCCCTGTGAGCTGTGGTGCACAGCATCTACCATCGCTGGACAGGGCCCTCT	1625
Qy	501	GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly	520
Db	1626	GGTCCCATCTCCGGCTTCACTACCAAGATAACACCCCTGAGGTGGAAAGTTCTGCCGGGC	1685
Qy	521	IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
Db	1686	ATCCTATTCTTGTGGGCTTGTCTCTTGTGGGTGTGGCCTGAGCCTGGCCACCTCTGGA	1745
Qy	541	ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp	560
Db	1746	AGGTGCTTACCACCTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT	1805
Qy	561	ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu	580
Db	1806	CCTGCCAACAGCATTCAGGCCAGCCCCACATGAGCAAGTACCTTGAGGGCCAGCCCTTT	1865
Qy	581	GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer	600
Db	1866	GGGACTTGGCCATCTCGAAGTGGAGAGATGAGCCCCCGCGGTATGGAGTCTCTCC	1925
Qy	601	GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr	620
Db	1926	CAGCCCCCGCCAGGCCACCGCCCGCTTGTCTGGGTATGAGAAGCACTTCTCTGCCACA	1985
Qy	621	ProGluLeuLeuGlyLeuLeuGlyProProArgProGlnValLeuAla	636
Db	1986	CCTGAGGAGCTGGGCTTCTTGGGGCCCCCGCCAGGCCACAGGTTCTTGCC	2033

RESULT 7

ADL91800

ID ADL91800 standard; cDNA; 3258 BP.

XX

AC ADL91800;

XX



Qy 241 AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro 260.  
Db 1144 AACCTCTGTGGAGCGCTTGGAGGAGAGAACTTGTCTTATGGAAGGCCCGCCAGGCCCC 1203  
Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280  
Db 1204 TGTGTGAGGTGAGCTACAAAGTCTGTGTCTTGGGTGTGAGGTCTGTGAGTTCAGAA 1263  
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
Db 1264 GGAATTACCTGCTGCTCCCTAATTCCTCCAGTGGGGGGGAGTGGCCAGGGTGTCCGCT 1323  
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
Db 1324 GTCAAGCCCAAGCTGGAGCCTCTCACCACCTCTCTTTGGTCTGCTTGGATTACGCC 1383  
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
Db 1384 TCTGCCCCCGTAGCGTGGCAGTCAGCAGCATCTGCGGAGCAGCGAGCTACTGTGTACC 1443  
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
Db 1444 TGGCAACCGGGCTTGGGAAACCACTGGAGCATGTAGTGGCTCGAGATGGGGAC 1503  
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
Db 1504 CCCCTGGAGAACTCAACTGGTCCGCTCCCGCTGGGAACCTCAGTGTCTGTACCA 1563  
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
Db 1564 GGGAAATTTCATGTCGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1623  
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluLeuAlaProLeuValGlyPro 420  
Db 1624 TTGGCTCTGCATCTCTGCTGGGGTTGAGGAGGAATTAGCACCCCTAGTGGGGCCA 1683  
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
Db 1684 ACGCTTTGGGACTTCAAGATGCCCTCCAGGACCCCGCCATAGCGTGGGAGAGGTC 1743  
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460  
Db 1744 CCAAGGCACCAAGCTTCAGAGCCACCTCACCACCTACACCTTGTGTGCACAGAGTGGAAAC 1803  
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
Db 1804 AGCCCTCCGTCTGCATGAATGTGAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1863  
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
Db 1864 CCTTGGGTCCCTGTGAGCTGTGGTGCACAGCATCTACCATGCTGGACAGGGCCCTCCT 1923  
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
Db 1924 GGTCCCATCTCCGGCTTCTATCACCAGATAACACCTCGAGTGGAAAGTTCTGCCGGC 1983  
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
Db 1984 ATCTATTCTTGTGGGCTGTGTCTCTGTGGGTGTGGCTGAGCCTGGCCACCTCTGGA 2043  
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
Db 2044 AGGTGCTACCACTAAGGCACAAAGTCTGCCCGCTGGTCTGGGAGAAAGTCTCTGAT 2103  
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
Db 2104 CCTGCCAACAGCAGTTCAGGCCAGCCCCACATGAGCAAGTACTGAGGGCCAGCCCTT 2163  
Qy 581 GlyAspLeuProIleLeuGluValGluMetGluProProValMetGluSerSer 600  
Db 2164 GGGGACTTGGCCATCTCGGAAGTGGAGAGATGAGCCCCCGCGGTATTGGAGTCTCTCC 2223

Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
Db 2224 CAGCCGCCCGAGGCCACCGCCCGCTTGACTCTGGGTATGAGAAGCACTTCTCTGCCACA 2283  
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
Db 2284 CCTGAGAGCTGGGCTTCTGGGGCCCCCGAGGCCACAGGTTCTGGCC 2331  
RESULT 8  
ADRI14162  
ID ADR14162 standard; DNA; 3258 BP.  
XX  
AC ADR14162;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human NF-kappaB pathway-associated gene SeqID163.  
XX  
KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;  
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
KW immunosuppressive; vulnery; gene therapy; immune disorder;  
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
KW viral infection; HIV-1; hepatitis B; hepatitis C; EBV; influenza;  
KW viral replication; host cell survival; evasion of immune response;  
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;  
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB;  
KW autoimmune disorder; hyper immune activity;  
KW aberrant acute phase response; hypercongenital condition; birth defect;  
KW necrotic lesion; wound; organ transplant rejection;  
KW aberrant signal transduction; proliferating disorder; cancer;  
KW HIV propagation; gene; ds; human.  
XX  
OS Homo sapiens.  
XX  
WO2004065577-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 13-JAN-2004; 2004WO-US000798.  
XX  
PR 14-JAN-2003; 2003US-0440068P.  
XX  
PR 12-MAY-2003; 2003US-0469757P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Nadler SG, Neubauer MG, Feder JN, Carman J;  
XX  
WIPI: 2004-562168/54.  
XX  
P-PSDB; ADRI14163.  
XX  
PT New isolated polynucleotides and polypeptides associated with NF-kappaB  
XX  
PT pathway, useful for diagnosing, treating, or preventing disorders or  
XX  
PT diseases associated with NF-kappaB pathway.  
XX  
PS Claim 1; SEQ ID NO 163; 237pp; English.  
XX  
CC This invention relates to the novel association of protein sequences (and  
XX  
CC the genes which encode them) to the NF-kappaB pathway. The invention may  
XX  
CC be useful for the production of compounds with an antiinflammatory,  
XX  
CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,  
XX  
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,  
XX  
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
XX  
CC vulnery activity or for gene therapy. The proteins and nucleotides are  
XX  
CC useful for diagnosing, preventing, treating, or ameliorating conditions  
XX  
CC or diseases associated with the NF-kappaB pathway. The condition is an  
XX  
CC immune disorder, an inflammatory disorder, an inflammatory disorder  
XX  
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
XX  
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
XX  
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
 CC immune activity, disorders related to aberrant acute phase responses,  
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,  
 CC organ transplant rejection, conditions related to organ transplant  
 CC rejection, disorders related to aberrant signal transduction,  
 CC proliferating disorders, cancers and HIV propagation in cells infected  
 CC with other viruses. The present sequence is that of a human gene which is  
 CC subject to the novel association with the NF-kappaB pathway of the  
 CC invention. Note: This sequence does not appear in the specification but  
 CC was obtained by the indexer from Genbank.  
 XX  
 SQ Sequence 3258 BP; 722 A; 942 C; 964 G; 630 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,23e-164 Length: 3258  
 Score: 3498.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

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QY	1	MetArgGlyValGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
DB	424	ATGCGGGAGGAGCGGGCGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGCGTGTG	483
QY	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln	40
DB	484	CCTCTGTTGTGGTGTCTTTTCAGCGGAGCGGTCCCGAGGAGCGCCGGGCCACTGCGAG	543
QY	41	CysTyrGlyValGlyProLeuGlyAspLeuAenCysSerTrpGluProLeuGlyAspLeu	60
DB	544	TGCTACGGAGTTGGACCTTGGCGGACTTGAATCGCTCGTGGGAGCCTCTTGGGACCTG	603
QY	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
DB	604	GGAGCCCCCTCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAAACAAACCCAGACT	663
QY	81	ValAlaValAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
DB	664	GTGGCAGTGGCAGCGGAGCTGGGTGGCCATCTCTCGGGAACAGCTCACCATGCT	723
QY	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
DB	724	GACAAACTCCTGTCTGGGGCACTAAGGCAGGCGACGCTCTCGGCCCCCGCTCTTCGNG	783
QY	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspPheSer	140
DB	784	AACCTAGAAACCCAAATGAAGCCAAACGCCGCCCGGCTGGGCGCTGACGTGACTTTTCC	843
QY	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
DB	844	GAGGATGACCCCTGGAGGCGACTGTCATTTGGGCCCCACCTACATGGCCATCTCAATAA	903
QY	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
DB	904	GTTCTCATCTGCCAGTTCCACTACCGAAGATGTACAGAGGCGGCGCTGGACCTGTCTGAA	963
QY	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
DB	964	CGGAGCTGAAGACCACTACCCCTGACCCCTGTGAGATCCAAGATTGGAGCTAGCCACT	1023
QY	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp	220
DB	1024	GGCTACAAAGTGTATGGCCGCTGCCGATGGAGAGAGAGGATTTGTGGGCGAGTGG	1083
QY	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240

DB	1084	AGCCCCATTTTCTCTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG	1143
QY	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPro	260
DB	1144	AACCTCTGTGGGACCCCTGGAGGAGGAACCTTGTCTTCTAATGAAGGCCCCAGGGCCC	1203
QY	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
DB	1204	TGTGTGCAAGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTCTGTGAGTGTGAGTCCAGAA	1263
QY	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
DB	1264	GGATTTACCTGTCTGTCTCCCTAATTCACGTGGGGCGGAGTGGGCCAGGGTGTCCGCT	1323
QY	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
DB	1324	GTCAACGCCACAAAGCTGGAGCCTCTCACCAACCTCTCTTTTGGTCTGCTTGGATTTCAGCC	1383
QY	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
DB	1384	TCTGCCCCCGTAGCGTGGCAGTCAGCAGCATCGCTGGGAGCAGCGAGCTACTGGTGACC	1443
QY	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
DB	1444	TGGCAACCGGGGCTGGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC	1503
QY	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
DB	1504	CCCCCTGGAGAAACTCACTGGGTCCGGCTTCCCCCTGGGAACCTCAGTGCTCTGTATCCA	1563
QY	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
DB	1564	GGGAATTTCACTGTCTGGGCTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC	1623
QY	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
DB	1624	TTGGCTCTCGCATCTCTCGTCTGGGGTTCAGGGAGGAATTTAGACACCCCTAGTGGGGCCA	1683
QY	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
DB	1684	ACGCTTTGGGACTCCAAGATGCCCTCCAGGAGCCCCCGCCCATAGCTGGGGAGAGTTC	1743
QY	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
DB	1744	CCAGGCGCACCGCTTCGAGGCCACCTCACCCACATACACCTGTGTGTCAGAGTGGAAACC	1803
QY	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
DB	1804	AGCCCCCTCGCTCGCATGAATGTAGTGGCAACACACAGAGTGTCAACCTGCTGACCTT	1863
QY	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
DB	1864	CCTTGGGTGCTGTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGAGGCCCTCTCT	1923
QY	501	GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly	520
DB	1924	GGTCCCATCTCCGGCTTCACTACAGATAACACCTCGAGGTGGAGATTTCTGCGGGGC	1983
QY	521	IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
DB	1984	ATCCTATTCTTGTGGGGCTTGTCTCTTGTGGGGTGTGGCTGAGCCTGAGCCTCTGGA	2043
QY	541	ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp	560
DB	2044	AGGTGCTACCTTAAAGGCACAAAGTGTGCCCCCTGGTCTGGGAGAAAGTTCTGTAT	2103
QY	561	ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu	580
DB	2104	CCTGCCAACAGCAGTTTCAGGCCAGCCCCACATGGAGCAAGTACCTGAGGCCAGCCCTT	2163
QY	581	GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer	600
DB	2164	GGGGACTTTGCCCATCTCGAAGTGGAGAGATGGAGCCCCCGCGGTTATGAGTCTCTCC	2223

Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
Dy 2224 CAGCCGCCAGGACCGCCGCTTACTCTGGGTATGAGAGCACTTCTGCCCCACA 2283  
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
Dy 2284 CCGAGGAGCTGGGCTTCTGGGGCCCCCAGGCGCACAGGTTCCTGGCC 2331

RESULT 9  
ABSS4548  
ID ABS54548 standard; cDNA; 2628 BP.  
AC ABS54548;  
XX 10-DEC-2002 (first entry)  
XX cDNA encoding human IL-12R-like subunit.  
XX IL-D80; human; gene; ss; cytokine; anti-inflammatory; haematopoietic;  
XX interleukin; IL-27; haematopoietic cell; immune system; inflammation;  
XX IL-12R-like subunit; interleukin 12 receptor like subunit.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 112..2022  
XX /\*tag= a  
XX /product= "IL-12R-like subunit"  
XX WO200268596-A2.  
XX 06-SEP-2002.  
XX 22-FEB-2002; 2002WO-US005493.  
XX 22-FEB-2001; 2001US-00791497.  
XX 30-NOV-2001; 2001US-00000776.  
XX (SCHE ) SCHERING CORP.  
XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;  
XX Dewaal Malefyt R, Cheung J;  
XX WPI: 2002-7066978/76.  
XX P-PSDB; ABG32294.  
XX New polynucleotide and its encoded antigenic polypeptide (IL-D80  
XX cytokine), useful for regulating hematopoietic cells, in developing new  
XX therapies, or for diagnosing or treating abnormal physiology, e.g.  
XX inflammations.  
XX Disclosure; Page 69-72; 74pp; English.  
XX This invention relates to the DNA and protein sequences of a new cytokine  
XX IL-D80. The protein of the invention may have antiinflammatory activity  
XX and may act as an IL-D80 modulator or an IL-27 modulator. The  
XX polynucleotide of the invention or its encoded polypeptide is useful for  
XX regulating the activation, development, differentiation or function of  
XX various cell types, e.g. haematopoietic cells. This polynucleotide or  
XX polypeptide is also useful in discovering and developing new lymphokines  
XX and their related receptor or receptor subunits, and in developing new  
XX therapies for a wide range of degenerative or abnormal conditions, which  
XX (in)directly involve the immune system or haematopoietic cells. The  
XX polynucleotide or polypeptide is useful in diagnosing or treating  
XX abnormal physiology or development, e.g. inflammations. The present  
XX sequence represents the cDNA encoding the human interleukin 12- receptor-  
XX like subunit protein of the invention  
XX SQ Sequence 2628 BP; 548 A; 778 C; 790 G; 511 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 2.82e-164 Length: 2628

Score: 3494.00 Matches: 635  
Percent Similarity: 99.84% Conservative: 0  
Best Local Similarity: 99.84% Mismatches: 1  
Query Match: 99.89% Indels: 0  
DB: 6 Gaps: 0  
US-10-088-950A-1 (1-636) x ABS54548 (1-2628)  
Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
Dy 112 ATGGGGGAGGAGGGGGCCCTTCTGGCTGTGGCCGTGCCAAGCTGGCGCTGCTG 171  
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
Dy 172 CCTCTGTGTGGTGTCTTTCCAGCGAGCGCTCCCGAGGCGAGCGCGGCCACTGCAG 231  
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60  
Dy 232 TGCTACGGAGTTGGACCCCTTGGGCGACTTGAATGCTCTGGGGAGCCCTCTTGGG 291  
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
Dy 292 GAGGCCCTCCCGATTACCTCCAGAGCCAAAGTACCGTTCCACAAACCCAGACT 351  
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
Dy 352 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGTCT 411  
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120  
Dy 412 GACAAACTCCTTGTCTGGGCGACTAAGGCGAGCGGCGCTCTCTGGCCCCCGCTTC 471  
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
Dy 472 AACCTAGAAACCCAAATGAAGCCAAAGCCCCCGCTGGGCGCTGACGTGGACTTTCC 531  
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
Dy 532 GAGGATGACCCCTGGGAGGCGACTGTCCATTGGGCCCCACCTACATGCCCATCTCA 591  
Qy 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
Dy 592 GTTCTGATCTGCCAGTTCCACTACCGAAGATGTCCAGAGCGCGCTGGACCTGCTG 651  
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
Dy 652 CCGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAAGATTGGAGTAGCC 711  
Qy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyLys 220  
Dy 712 GGCTACAAAGTGTATGGCGCTGCCGATGGAGAAAGAGAGGATTGTGGGGCGAGTGG 771  
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
Dy 772 AGCCCCATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAG 831  
Qy 241 AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
Dy 832 AACCTCTGTGGGAGCGCTGGAGGAGGAAACCTTGTCTTATGGAAGGCCCCAGGGCCC 891  
Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280  
Dy 892 TGTGTGCAAGTACAGCTACAAAGTCTGGTTCTGGGTTGGAGTCTGTAGCTGAGTCC 951  
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
Dy 952 GGAATTAACCTGCTGCTCCCTAAATTCCAGTGGGCGGAGTGGCGGCGTGTGCGCT 1011  
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
Dy 1012 GTCAAGCCCAAGCTGGGAGCGCTCTCACCACCTCTCTTGTGCTGTGGATTACGCC 1071  
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340





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Oy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 172 CCTCTGTGTGGTGTCTTTCCAGCGGACGGTCCCCAGGCGCAGCGCGGCGCCACTGCAG 231
Oy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnGlySerTrpGluProLeuGlyAspLeu 60
Db 232 TGCTACGAGGTGACCCCTCGGGGACCTTGAACCTGCTCGTGGGAGCCCTCTTGGGGAGCTG 291
Oy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db 292 GGAGCCCTCCGAGTTACACTCCAGAGCCAAAGTACCGTTCCAAACAACCCAGACT 351
Oy 81 ValAlaValAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 352 GTGGCAGTGGCAGCCGAGCGAGCTGGGTGGCCATTCCTCGGGAACAGCTCACCATGTCT 411
Oy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
Db 412 GACAAACTCCTTGTCTGGGGCACTAAGCGAGCGAGCCCTCTCTGGCCCCCGCTCTCGTG 471
Oy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 472 AACCTAGAACCCAAATGAAGCCAAACGCCCCCGGCTGGGCCCTGACGTGGACTTTTCC 531
Oy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
Db 532 GAGGATGACCCCTGGAGGCCACTGTCCATTTGGGCCCCACCCTACATGGCCATCTCATAA 591
Oy 161 ValLeuLeuCysGlnPheHisTyrArgArgCysGlnGluAlaIleTrpThrLeuLeuGlu 180
Db 592 GTTCTGTATCTGCCAGTTCACATACCGAAGATGTGAGGAGCGCGCTGACCCCTCTGGAA 651
Oy 181 ProGluLeuLysThrIleProLeuThrProValGluLeuGlnAspLeuGluAlaThr 200
Db 652 CCGAGCTGAAGACCATACCCCTGACCCCTGTGAGATCCAAAGATTTGGAGCTAGCCACT 711
Oy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
Db 712 GGCTACAAAGTGTATGGCCGCTGCGGATGGAGAAAGAGAGGATTTGTGGGGCGAGTGG 771
Oy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
Db 772 AGCCCCATTTTGTCTTCCAGACACCGCTTCTCTCCAAAGATGTGTGGGTATCAGGG 831
Oy 241 AsnLeuCysGlyThrProGlyGlyGluLeuProLeuLeuTrpLysAlaProGlyPro 260
Db 832 AACCTCTGTGGAGCGCTTGAGGAGAGAACCTTTGCTTATGAAAGGCCCCAGGGGCC 891
Oy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
Db 892 TGTGTGAGGTGAGCTACAAAGTCTGTTCTGGGTGGAGGTCTGTGAGCTGAGTCCAGAA 951
Oy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
Db 952 GGAATTAACCTGCTGCTGCTCCCTAAATCCAGTGGGGCGAGTGGGCGAGGGTCTCGCT 1011
Oy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
Db 1012 GTCAACGCCCAAGCTGGAGCCCTCTCACAACCTCTCTTTGGTCTGCTTGGATTCAGCC 1071
Oy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
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Oy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
Db 1132 TGGCAACCGGGCGCTGGGGAACCACTGGAGCATGTAGTACCTGGGCTCGAGATGGGAC 1191
Oy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
Db 1192 CCCCTGGAGAACTCAACTGGGTCCGCTTCCCCCTGGGAACCTCAGTGTCTGTACCA 1251
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Oy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1252 GGGATTTTCACTGTGCGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1311
Oy 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1312 TTGGCCCTCTCATCTCTCCGTCTGGGGTTTCCAGGGAGGAATTAGCACCCCTAGTGGGCCA 1371
Oy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaIleTrpGlyGluVal 440
Db 1372 ACGTTTGGGCACTCCCAAGATGCCCTCCAGGGACCCCGCCCATAGGCTGGGGAGAGTC 1431
Oy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1432 CCAAGGCACCACTTTCAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGAAC 1491
Oy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1492 AGCCCTCTCCGTCTGCAATGAGTGGAGTGGCAACACACAGAGTGTACCTCTGCCTGACTT 1551
Oy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1552 CCTTGGGTCCTCTGTAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1611
Oy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1612 GGTCCCATCTCCGGCTTCATCTACAGATAACACCCCTGAGGTGGAAGTTCTGCCGGGC 1671
Oy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1672 ATCCTATTCTTGTGGGCTTGTTCCTGTGGGTGTGGCTGAGCCTGGCCACCTCTGGA 1731
Oy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1732 AGTGCTTACCATCCCTAAGGCACAAGTGTCTCCCGCTGGGTCTGGGAAAGTTCTCTGAT 1791
Oy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1792 CCTGCCAACAGCAGTTTCAGGCCAGCCACATGAGCAAGTACCTGAGGCCAGCCCTT 1851
Oy 581 GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer 600
Db 1852 GGGGACTTGGCCATCTCTGGAAGTGGAGGAGATGGAGCCCCCGCGGTATGGAGTCTCTCC 1911
Oy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1912 CAGCCGCCAGGCCACCGCCCGCTTGACTCTGGGTATGAGAAGCACTTCTCTGCCCA 1971
Oy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1972 CCTGAGGAGCTGGGCCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2019

RESULT 11
ABX10922
ID ABX10922 standard; cDNA; 2628 BP.
XX
AC ABX10922;
XX
DT 29-APR-2003 (first entry)
XX
DE Human interleukin-12 R beta 2 subunit homologue WSX-1/TCCR, cDNA.
XX
KW Human; cytokine; IL-D80; IL-27; interleukin D80; interleukin 27;
XX inflammation; autoimmune disorder; drug screening; cell activation;
XX cell development; cell differentiation; gene; ss; WSX-1/TCCR;
XX interleukin-12 R beta 2 subunit.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 112..2022
FT /*tag= a
FT /product= "WSX-1/TCCR"
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/note= "Interleukin-12 R beta 2 subunit homologue"

FT	US2002164609-A1.	
XX	07-NOV-2002.	
XX	30-NOV-2001; 2001US-00000776.	
XX	30-JUL-1999; 99US-0146581P.	
PR	06-AUG-1999; 99US-0147763P.	
PR	27-JUL-2000; 2000US-00627897.	
PR	22-FEB-2001; 2001US-00791497.	
XX	(TIMA/) TIMANS J C.	
PA	(PFLA/) PFLANZ S K.	
PA	(KAST/) KASTELEIN R A.	
PA	(BAZA/) BAZAN J F.	
PA	(RENN/) RENNICK D.	
PA	(MALE/) DE WAAL MALEFYT R.	
PA	(CHEU/) CHEUNG J.	
XX	Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;	
PI	De Waal Malefyt R, Cheung J;	
XX	WPI; 2003-275305/27.	
DR	P-PSDB; ABG75880.	
XX	New isolated or recombinant cytokine or composite cytokine genes and	
PT	proteins (e.g. interleukin D80 or interleukin 27), useful for diagnosing	
PT	or treating e.g. inflammation or autoimmune disorders, or for regulating	
PT	cell biology.	
XX	Disclosure; Page 28-30; 37pp; English.	
XX	The invention describes an isolated or recombinant polynucleotide, which	
CC	encodes an antigenic polypeptide. The polynucleotide, polypeptide or	
CC	binding compound is useful for diagnosing or treating IL-D80 or IL-27	
CC	mediated conditions, e.g. inflammation or autoimmune disorders. These are	
CC	also useful in drug screening. The polynucleotide, polypeptide,	
CC	antibodies or compositions are also useful for controlling biology and	
CC	physiology of mammalian cells (e.g. cells of a mammalian immune system),	
CC	or for regulating the activation, development, differentiation, and	
CC	function of various cell types (e.g. hematopoietic or lymphoid cells).	
CC	This sequence encodes the human interleukin-12 R beta 2 subunit homologue	
CC	WSX-1/TCR used with human interleukin D80 (IL-D80) or 27 (IL-27)	
CC	sequences to create a composite cytokine	
XX	Sequence 2628 BP; 548 A; 778 C; 790 G; 511 T; 0 U; 1 Other;	
SQ		
Alignment Scores:		
Pred. No.:	2,82e-164	Length: 2628
Score:	3494.00	Matches: 635
Percent Similarity:	99.84%	Conservative: 0
Best Local Similarity:	99.84%	Mismatches: 1
Query Match:	99.89%	Indels: 0
DB:	8	Gaps: 0
US-10-088-950A-1 (1-636) x ABX10922 (1-2628)		
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DB	112 ATGCGGGAGGAGGGGGCGCCCTTTCTGGCTGTGGCGCGCTGCCAAGCTGGCGTGTG 171	
QY	21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40	
DB	172 CTCTGTGTGGTGGTGTCTTTCAGCGACGCGTCCCGAGGAGCGCCCGGCGCACTGCGAG 231	
QY	41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60	
DB	232 TGCTACGGAGTTGGACCCCTTGGCGGCTTGAACCTGCTGTGGGAGGCTCTTGGGAGCCTG 291	
QY	61 GlyAlaProSerGlnLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80	

Db	292	GGAGCCCCCTCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAAACAAAACCCAGACT	351
QY	81	ValAlaValAlaAlaGlyArgSerTrpValAlaAlaLeuProArgGluGlnLeuThrMetSer	100
DB	352	GTGGCAGTGGCAGCCGAGCGAGCTGGGTGGCCATTCTCTCGGGAACAGCTCACCATGTCT	411
QY	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
DB	412	GACAACTCTTGTCTGGGCACTAAGGCAGCCAGCCCTCTCTGGCCCCCTCTTCGTG	471
QY	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
DB	472	AACCTAGAACCCAAATGAAGCCAAACGCCCGCGCTGGGCGCTCGAGCTGACTTTTCC	531
QY	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProTrpProSerHisLys	160
DB	532	GAGGATGACCCCTCGAGGCCACTGTCCATTGGGCCCCCACCCTACATGGCCATCTCATAA	591
QY	161	ValLeuLeuCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
DB	592	GTTCTGATCTGCCAGTTCCTACTACCGAAGATGTCAGGAGGGCGCTGGACCCCTGCGAA	651
QY	181	ProGluLeuLysThrIleProLeuThrProValGluLeuGlnAspLeuGluLeuAlaThr	200
DB	652	CGGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAGATTGGAGCTAGCCACT	711
QY	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
DB	712	GGCTACAAGTGTATGGCGCTGCCGATGGAGAAGAAGAGGATTTGTGGGGCGAGTGG	771
QY	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
DB	772	AGCCCCCATTTTGTCTTCCAGACACCGCTCTCTCCAAAAGATGTGGGTATCAGG	831
QY	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
DB	832	AACCTCTGTGGGACCCCTGGAGGAGAGGAACCTTTGTCTTATGAAGGCCCCAGAGGCC	891
QY	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
DB	892	TGTGTGAGGTGAGGTACAAAGTCTGGTCTGGGTGGAGGTGCTGAGTGTAGTCCAGAA	951
QY	281	GlyIleThrCysCysSerSerLeuLeuProSerGlyAlaGluTrpAlaArgValSerAla	300
DB	952	GGATTTACCTGCTGCTGCTCCCTAATCCAGTGGGCGGAGTGGGCCAGGGTCTCCGCT	1011
QY	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
DB	1012	GTCAACGCCCAAGCTGGGAGCCCTCTCCAAACCTCTCTTTGGTCTGCTTGGATTTCAGCC	1071
QY	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
DB	1072	TCTGCCCCCGTAGGCTGGCAGTACGAGCATCGCTGGGAGCAGCGAGCTACTGTGTGACC	1131
QY	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
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QY	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
DB	1192	CCCCCTGGAGAACTCACTGGGTCCGGCTTCCCCCTGGGAACCTCAGTGTCTGTFTACCA	1251
QY	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
DB	1252	GGGAATTTCACTGTGGGGTCCCTTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC	1311
QY	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
DB	1312	TTGGCTCTGCATCTCCGCTGTGGGGTTTCAAGGAGGAATTAGCACCCCTAGTGGGGCA	1371
QY	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
DB	1372	ACGCTTTGGCGACTCAAGATGCCCTCCAGGAGCCCCCGCCCATAGCGTGGGAGAGGTC	1431



Db 421 GAGGATGACCCCTGGAGGCCACTGTCATTTGGGGCCCCACCTACATGGCCATCTCATAAA 480  
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Db 481 GTTCTGATCTGCCAGTTCACATACCAAGATGTGAGAGGGCCCTGGACCTGTCTGGAA 540  
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
Db 541 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAGATTTGGAGTAGCCACT 600  
Qy 201 GlyTyLysValTyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220  
Db 601 GGTACAAAGTGTATGGCGCTGCCGATGGAGAGAGAGATTTGGGGCGAGTGG 660  
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
Db 661 AGCCCCATTTGTCCTTCAGACACCGCCTTGTCTCCAAAGATGTGGGTATACAGG 720  
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
Db 721 AACCTCTGTGGAGCGCTGGAGGAGAGAACCTTTGCTTATGGNAGGCCCCAGGGCCC 780  
Qy 261 CysValGlnValSerTyLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
Db 781 TGTGTGAGGTGAGCTACAAAGTCTGGTTCTGGTTGGAGGTCTGTGAGCTGAGTCCAGAA 840  
Qy 281 GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
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Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
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Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
Db 961 TCTGCCCCCTAGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1020  
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Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
Db 1201 TTGGCTCTGCAATCTCTGGGGTTCAGGGAGAAATAGACCCCTAGTGGGGCCA 1260  
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
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Db 1501 GGTCCCATCTCCGGCTTCACTTACCAGATAACACCTGAGGTGGAAAGTCTTCTGCGGGC 1560

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Db 1561 ATCCTATTCTTGTGGGGCTTGTCTCTGTGGGTGTGGCTGAGCTGGCCACCTCTGA 1620  
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Db 1621 AGGTGCTACCACTAAGGCAAAAGTGTGCCCCCTGGTCTGGGAGAAAGTCTCTGAT 1680  
Qy 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
Db 1681 COTGCAACAGCAGTTCAGGCCAGCCCACTGGAGCAAGTACCTGAGGCCAGCCCTT 1740  
Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600  
Db 1741 GGGGACTTGCCCATCTCGAAGTGGAGAGATGGAGCCCCCGCGTTATGGAGTCTCTCC 1800  
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyTrpGluLysHisPheLeuProThr 620  
Db 1801 CAGCCCCGCCAGGCCACCGCCGCTTGACTCTGGGTATGAGAGCACTTCTCTGCCACA 1860  
Qy 621 ProGluGluLeuGlyLeuGlyProProArgProGlnValLeuAla 636  
Db 1861 COTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTCTCTGGCC 1908  
RESULT 13  
ACC46162  
ID ACC46162 standard; cDNA; 2350 BP.  
XX ACC46162;  
XX 02-JUN-2003 (first entry)  
DE Human dithp receptor-encoding cDNA.  
XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
KW cancer; cell proliferative disorder; autoimmune disorder;  
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging; receptor; gene;  
SS.  
XX Homo sapiens.  
OS  
XX WO200297031-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 27-MAR-2002; 2002WO-US010056.  
XX  
XX 28-MAR-2001; 2001US-0279619P.  
PR 29-MAR-2001; 2001US-0280067P.  
PR 29-MAR-2001; 2001US-0280068P.  
PR 16-MAY-2001; 2001US-0291280P.  
PR 17-MAY-2001; 2001US-0291829P.  
PR 17-MAY-2001; 2001US-0291849P.  
PR 19-JUN-2001; 2001US-0299428P.  
PR 20-JUN-2001; 2001US-0299776P.  
PR 20-JUN-2001; 2001US-0300001P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David WH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX WPI; 2003-129518/12.  
DR P-PSDB; ABR41219.  
XX

PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
PT test compound which specifically binds to a polypeptide encoded by human  
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.

Claim 2; SEQ ID NO 83; 591pp; English.

The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic disorders; neurological disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a dithp cDNA encoding a DITHP protein, which has receptor activity. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

SQ Sequence 2350 BP; 455 A; 712 C; 719 G; 464 T; 0 U; 0 Other;

Alignment Scores:		
Pred. No.:	Length:	2350
Score:	Matches:	633
Percent Similarity:	Conservative:	1
Best Local Similarity:	Mismatches:	2
Query Match:	Indels:	31
DB:	Gaps:	1
US-10-088-950A-1 (1-636) x ACC46162 (1-2350)		

Qy	1	Met	Arg	Gly	Gly	Arg	Gly	Ala	Pro	Phe	Trp	Leu	Trp	Pro	Leu	Pro	Lys	Leu	Ala	Leu	Leu	20
Db	49	AT	G	G	G	G	G	A	G	G	G	C	T	T	T	G	G	C	G	C	T	107
Qy	21	Pro	Leu	Leu	Trp	Val	Leu	Phe	Gly	Arg	Thr	Arg	Pro	Gln	Gly	Ser	Ala	Agly	Pro	Leu	Gln	40
Db	108	C	C	T	C	T	G	T	G	G	T	C	T	T	T	C	A	G	C	G	C	166
Qy	41	Cys	Tyr	Gly	Val	Gly	Pro	Leu	Gly	Asp	Leu	Asn	Cys	Ser	Trp	Glu	Pro	Leu	Gly	Asp	Leu	60
Db	167	T	G	C	T	A	C	G	A	G	T	T	G	A	C	C	T	T	G	G	A	226
Qy	61	Gly	Ala	Pro	Ser	Glu	Leu	His	Leu	Gln	Ser	Gln	Lys	Tyr	Arg	Ser	Asn	Lys	Thr	Gln	80	
Db	227	G	A	G	G	C	C	C	T	C	G	A	G	T	T	A	C	T	C	A	G	286
Qy	81	Val	Ala	Val	Ala	Ala	Gly	Arg	Ser	Trp	Val	Ala	Ile	Pro	Arg	Glu	Gln	Leu	Thr	Met	Ser	100
Db	287	G	T	G	C	A	G	T	G	G	T	G	G	C	A	T	T	C	T	C	G	346
Qy	101	Asp	Lys	Leu	Leu	Val	Trp	Gly	Thr	Lys	Ala	Gly	Gln	Pro	Leu	Trp	Pro	Pro	Val	Phe	Val	120
Db	347	G	A	C	A	A	C	T	C	T	T	G	T	C	T	G	G	A	G	C	C	406

Qy	121	AsnLeuGluThrGln	-----MetLysProAsnAlaPro	131
Db	407	AACTAGAAACCCAAAGTAACGTGGCAGGAGGTGGCGCTCTATGCGGGTGGGTGCTC	466	
Qy	126	-----	-----	
Db	467	TTGGAGGGCGTGCTCACTACACCTAGTTTCCCTTCCCAGTGAAGCCAAACGCCGCC	526	
Qy	132	ArgLeuGlyProAspValAspPheSerGluAspAspProLeuGluAlaThrValHisTrp	151	
Db	527	CGGCTGGCCCTGACGTGGACATTTCGAGAGTAGACCCCTCGAGGGCCACTGTCATTTGG	586	
Qy	152	AlaProProThrTrpProSerHisLysValLeuLeuCysGlnPheHisTyArgAArgCys	171	
Db	587	GCSCCACTACATGGCCCATCTCAATAAGTTCTGATCTGCCAGTTCCACTACCGAAGATGT	646	
Qy	172	GlnGluAlaAlaTrpThrLeuLeuGluProGluLeuLysThrLeuProLeuThrProVal	191	
Db	647	CAGAGCGGCCCTGGACCCCTGCTGGAAACCGGAGCTGAAGACCATACCCCTGACCCCTGTT	706	
Qy	192	GluIleGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGlu	211	
Db	707	GAGATCCAAAGATTGGAGCTAGCCACTGGCTACAAGATGATGCGCGCTGCCGATGGAG	766	
Qy	212	LysGluGlnAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSer	231	
Db	767	AAAGAAGAGATTGTGGGGCGAGTGGAGCCCATTTGTCTCTCCAGACACCGCCTTCT	826	
Qy	232	AlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluPro	251	
Db	827	GCCTCCAAAGATGTGTGGGTATCAGGGAAACCTCTGTGGGACGCGCTGGAGAGGAAACCT	886	
Qy	252	LeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrp	271	
Db	887	TTGCTTCTATGGAAGGCCCGCGCCCTGTGTGCAGGTGAGCTACAAGTCTGGTCTGTGG	946	
Qy	272	ValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysCysSerLeuLeuProSer	291	
Db	947	GTGGAGTCTGTCAGCTGAGTCCAGAAGGAATTAACCTGTCTGTCTCCCTAAATCCAGT	1006	
Qy	292	GlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAsn	311	
Db	1007	GGGCGGAGTGGGCCAGGGGTGCCGTGTCAACGCCACCAAGCTGGAGGCGCTCTCACCAAC	1066	
Qy	312	LeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerIle	331	
Db	1067	CTCTCTTTGGTCTGCTTGATTCAAGCTCTGCCCCCGGTAGCGTGGCAGTCAGCAGATC	1126	
Qy	332	AlaGlySerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHis	351	
Db	1127	GCTGGGAGCACGAGCTACTGTGTGACTGCGCAACCGGGGCCCTGGGGAAACCATCTGGAGCAT	1186	
Qy	352	ValValAspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuPro	371	
Db	1187	GTAGTGACTGGGCTCGAGATGGGGACCCCTCGAGAAACTCAACTGGGTTCGGCTTCCC	1246	
Qy	372	ProGlyAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIle	391	
Db	1247	CCTGGGAACTCTAGTGTCTGTATACAGGGAATTTCACTGTGGGGTCCCTCATCGAATC	1306	
Qy	392	ThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArg	411	
Db	1307	ACTGTGACGCGACTCTCTGCTTCAGGCTTGGGCTCTGCACTCTCCGTCTGGGGTTTCAGG	1366	
Qy	412	GluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGly	431	
Db	1367	GAGGAATTAGACCCCTAGTGGGGCCAAACGCTTTGGCGACTCCAAGATGCCCTCCAGG	1426	
Qy	432	ThrProAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHis	451	
Db	1427	ACCCCGCCNATACGTGGGAGAGGTCCCAAGGCACAGCTTCGTGAGGCCACTTACCCAC	1486	
Qy	452	TyrThrLeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsn	471	

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Db 1487 TACACCTTGTGTGCAGAGTGAACAGCCCTCGTCTGTCATGAATGTGAGTGGCAAC 1546
Qy 472 ThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAla 491
Db 1547 ACACAGAGTGTACCCCTGCTGACCTTCCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCA 1606
Qy 492 SerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAspLeu 511
Db 1607 TCTACCATCGCTGGAGAGGGCCCTCTGTGTCCATCTCCGGCTTCATCTACCAATAC 1666
Qy 512 ThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuLeuLeuGly 531
Db 1667 ACCCTGAGGTGAAAGTTCTGCGGGCATCTATTCTTGTGGGCTTGTCTGTGGGG 1726
Qy 532 CysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArgHisLysValLeuPro 551
Db 1727 TGTGGCTGAGCTGGCCACCTCTGGAAGGTGCTACCACTAAGGCACAAAGTGTCTGCC 1786
Qy 552 ArgTrpValTrpGluLysValProAspProAlaAsnSerSerSerGlyGlnProHisMet 571
Db 1787 CGTGGGTCTGGAGAAAGTTCTGTATCTCTGCCAACAGCAGTTTCAGGCCAGCCCAATG 1846
Qy 572 GluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGluMet 591
Db 1847 GAGCAAGTACCTGAGCCAGCCCTTGGGACTTGGCCATCTTGGAACTGGAGGATG 1906
Qy 592 GluProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeuAspSer 611
Db 1907 GAGCCCCCGGGTATGGAGTCTCCAGCCGCGCCAGCCAGCCAGCCCGGCTTGACTCT 1966
Qy 612 GlyTyrGluLysHisPheLeuProThrProGluGluLeuGlyLeuLeuGlyProProArg 631
Db 1967 GGTATGAGAAGACACTTCTGCCACACCTGAGGAGCTGGGCTTCTGGGGCCCCCAGG 2026
Qy 632 ProGlnValLeuAla 636
Db 2027 CCACAGTTCTGGCC 2041

RESULT 14
AAT94119
ID AAT94119 standard; cDNA; 2368 BP.
XX
AC AAT94119;
XX
DT 22-MAY-1998 (first entry)
XX
DE Human haematopoietic cytokine receptor Zcytor1 cDNA.
XX
KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;
XX cancer diagnosis; agonist; antagonist; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 23..1759
FT /*tag= a
FT /product= "Zcytor1"
XX
XX WO9744455-A1.
XX
XX
XX 27-NOV-1997.
XX
XX 19-MAY-1997; 97WO-US008502.
XX
XX 23-MAY-1996; 96US-00653740.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
XX WPI; 1998-018509/02.
XX
XX P-PSDB; AAW33398.

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XX
PT Haematopoietic cytokine receptor - useful for ligand detection, and
PT pathological condition diagnosis.
XX
PS Claim 13; Page 39-43; 86pp; English.
XX
CC The present sequence encodes the human haematopoietic cytokine receptor
CC Zcytor1, useful for ligand detection, and pathological condition
CC diagnosis, including cancer. Receptor agonists of the protein can be used
CC to stimulate the proliferation and development of target cells in vitro
CC and in vivo. The agonists can stimulate cell mediated immunity and
CC lymphocyte proliferation, to treat infection involving immunosuppression,
CC e.g. viral infections. They may also be used to suppress tumours, induce
CC cytotoxicity, treat leukaemias and enhance the regeneration of the T-
CC cell repertoire after bone marrow transplantation. Antagonists of the
CC protein may be used to suppress the immune system, treat autoimmune
CC diseases, including rheumatoid arthritis, multiple sclerosis and diabetes
CC mellitus. Immune suppression caused by the antagonists can also be used
CC to reduce rejection of tissue or organ transplants and grafts, and to
CC treat T-cell specific leukaemias and lymphomas
XX
SQ Sequence 2368 BP; 506 A; 688 C; 701 G; 473 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 2,82e-147 Length: 2368
Score: 3150.00 Matches: 578
Percent Similarity: 90.88% Conservative: 0
Best Local Similarity: 90.88% Mismatches: 0
Query Match: 90.05% Indels: 58
DB: 2 Gaps: 1

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US-10-088-950A-1 (1-636) x AAT94119 (1-2368)

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Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 23 ATGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 82
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 83 CCTCTGTTGTGGTGCTTTTTCAGCGGAGCGGCTCCAGGGAGCGCGGGGCATCTGCAG 142
Qy 41 CystGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 143 TGCTACGGAGTTGGACCTTGGCGACTTGAACCTCTCGTGGAGGCTCTTGGGACCTG 202
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db 203 GGAGCCCCCTCCGAGTTACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT 262
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 263 GTGGCAGTGGCAGCGGAGCGGAGCTGGTGGCCATCTCTCGGGAACAGCTACCATGCT 322
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
Db 323 GACAAACTCCTTGTCTGGGGCACAATAAGCAGCCAGCCTCTCTGGCCCCCGCTCTCGNG 382
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 383 AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGGCTGGGCGCTGAGCTGTTTCC 442
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
Db 443 GAGGATGACCCCTCTGGAGGCCACTGTTCATTGGGGCCCCCACCCTACATGGCCATCTATAA 502
Qy 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaThrThrLeuLeuGlu 180
Db 503 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTCCAGGAGGCGGCTGGACCTGTGGAA 562
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
Db 563 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTAGATCCAAAGATTGGAGTAGCCACT 622

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QY GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAapLeuTrrpGlyGluTrrp 220  
DB GCCTACAAAGTGTATGGCCGCTGCGGATGAGAAAGAGAGATTTGTGGGGGAGTGG 682  
QY SerProLeuLeuSerPheGlnThrProProSerAlaProLysAapValTrrpValSerGly 240  
DB AGCCCAATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 742  
QY AenLeuGlyThrProGlyGlyGluGluProLeuLeuLeuTrrpLysAlaProGlyPro 260  
DB AACCTCTGTGGAGCGCTGAGGAGAGAACTTTGCTTCTATGGAAGGCCCCAGGGCCC 802  
QY CysValGlnValSerTyrLysValTrrpPheTrrpValGlyArgGluLeuSerProGlu 280  
DB TGTGTGAGGTGAGCTACAAAGTCTGGGTCTGGGTGAGGTGAGTCTGAGTCCAGAA 862  
QY GlyTrrThrCysCysSerLeuLeuProSerGlyAlaGluTrrpAlaAatqValSerAla 300  
DB GGAATTACCTGCTGCTGCTTCCCTAATTCCTAGTGGGGGGAGTGGCCAGGGTGTCCGCT 922  
QY ValAenAlaThrSerTrrpGluProLeuThrAenLeuSerLeuValCysLeuAapSerAla 320  
DB GTCAAGCCCAACAGCTGGAGCCCTCTACCAACCTCTCTTTGGTCTGCTTGGATTACGCC 982  
QY SerAlaProArgSerValAlaValSerSerLeuAlaGlySerThrGluLeuLeuValThr 340  
DB TCTGCCCCCGTAGCTGGCAGTCAGCAGCATCGCTGGAGCAGCAGCTACTGCTGACC 1042  
QY TrrpGlnProGlyProGlyGluProLeuGluHisValValAapTrrpAlaAatqAapGlyAap 360  
DB TGGCAACCGGGGCTGGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGGAC 1102  
QY ProLeuGluLysLeuAenTrrpValArgLeuProProGlyAenLeuSerAlaLeuLeuPro 380  
DB CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTCGGAACTCAGTCTCTGTACCA 1162  
QY GlyAenPheThrValGlyValProTrrpArgThrValThrAlaValSerAlaSerGly 400  
DB GGGAAATTTCACTGCGGGTCCCTATCGAATCACTGTGACCGAGTCTCTGCTTCAGGC 1222  
QY LeuAlaSerAlaSerValTrrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
DB TTGGCCCTGTCATCTCCGTCTGGGGTTCAGGAGGAATTAGCACCCCTAGTGGGGCCA 1282  
QY ThrLeuTrrpArgLeuGlnAapProGlyThrProAlaLeuAlaTrrpGlyGluVal 440  
DB ACGCTTTGGGACCTCAAGATGCCCTCCAGGACCCCGCCATAGCGTGGGAGAGTTC 1342  
QY ProArgHisGlnLeuArgGlyHisLeuThrHisTrrpThrLeuCysAlaGlnSerGlyThr 460  
DB CCAAGGCACCAAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGAACC 1402  
QY SerProSerValCysMetAenValSerClyAenThrGlnSerValThrLeuProAapLeu 480  
DB AGCCCTCCGCTCTCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCTGACCTT 1462  
QY ProTrrpGlyProCysGluLeuTrrpValThrAlaSerThrThrLeuAlaGlyGlnGlyProPro 500  
DB CCTTGGGGTCCCTGTGAGCTGTGGGTGACGATCTACCATCGCTGACAGGGCCCTCTCT 1522  
QY GlyProLeuArgLeuHisLeuProAapAenThrLeuArgTrrpLysValLeuProGly 520  
DB GGTCCCATCTCCGGCTCTCATACAGATAACACCTGAGGTGAGAAAGTCTTCTGCGGGC 1582  
QY IleLeuPheLeuTrrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
DB ATCCTATTCTTGTGGGGCTTGTCTCTGTGGGGTGGCTGAGCTGGCCACCTCTGGA 1642  
QY ArgCysTrrHisLeuArgHisLysValLeuProArgTrrpValTrrpGluLysValProAap 560  
DB AGTGTCTACCACTTACGACCAAAAGTACTGCCCCGCTGGGTCTGGGAGAAAGTCTCTGAT 1702  
QY ProAlaAenSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580

DB ||||| 1703 CCTCCCAACAGCATTCAC----- 1720  
QY 581 GlyAapLeuProLeuGluValGluMetGluProProValMetGluSerSer 600  
DB 1720 ----- 1720  
QY 601 GlnProAlaGlnAlaThrAlaProLeuAapSerGlyTyrGluLysHisPheLeuProThr 620  
DB 1720 ----- 1720  
QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
DB 1721 -----GGCCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 1756  
RESULT 15  
ADR20078  
ID ADR20078 standard; cDNA; 1835 BP.  
XX  
AC ADR20078;  
XX  
XX 07-OCT-2004 (first entry)  
XX  
DE Human immune response associated protein (IRAP) cDNA, seq id 38.  
XX  
KW Neuroprotective; anorectic; cytostatic; gene therapy;  
KW human immune response associated protein; IRAP; immune system;  
KW neurological; developmental; muscle; cell proliferative; disorder;  
KW lipid metabolism; obesity; breast; colon; lung; ovarian; prostate;  
KW cancer; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004048550-A2.  
XX  
PD 10-JUN-2004.  
XX  
XX 25-NOV-2003; 2003WO-US038178.  
XX  
XX 26-NOV-2002; 2002US-0429442P.  
XX 27-NOV-2002; 2002US-0429839P.  
XX 13-JAN-2003; 2003US-0439946P.  
XX 07-FEB-2003; 2003US-0446182P.  
XX (INCY-) INCYTE CORP.  
XX  
XX Tran UK, Richardson TW, Becha SD, Elliott VS, Swarnakar A;  
PI Lee SY, Ramkumar J, Wang JT, Chien D, Murage J, Gera M, Marquis JP;  
PI Chawla NK, Nakamura LL, Kable AE;  
XX  
DR WPI; 2004-450368/42.  
DR P-PSDB; ADR20046.  
XX  
XX New immune response associated protein, useful in diagnosing, treating,  
PT or preventing obesity, cancer, immune system, neurological,  
PT developmental, muscle, or cell proliferative disorders, or disorders of  
PT lipid metabolism.  
XX  
PS Claim 5; SEQ ID NO 38; 199pp; English.  
XX  
XX The invention relates to an isolated polypeptide with human immune  
CC response associated protein (IRAP) activity. Further disclosed are  
CC polynucleotides encoding the polypeptides of the invention. The  
CC polypeptides, polynucleotides, composition, and methods are useful in  
CC diagnosing, treating, or preventing immune system, neurological,  
CC developmental, muscle, or cell proliferative disorders, disorders of  
CC lipid metabolism, obesity, and breast, colon, lung, ovarian, or prostate  
CC cancer. The current sequence represents a human immune response  
CC associated protein encoding cDNA.  
XX  
SQ Sequence 1835 BP; 331 A; 568 C; 568 G; 368 T; 0 U; 0 Other;  
Alignment Scores:

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Pred. No.: 4,06e-147 Length: 1835
Score: 3144.50 Matches: 579
Percent Similarity: 91.37% Conservative: 3
Best Local Similarity: 90.89% Mismatches: 1
Query Match: 89.89% Indels: 54
DB: 12 Gaps: 1

US-10-088-950A-1 (1-636) x ADR20078 (1-1835)

QY 1 MetArgGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 37 ATGCGGGAGGAGGCGGCCCTTTCTGGCTGTGGCCGCTGCCAAGCTGGCGTGTG 96
QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 97 CCTCTGTGTGGGTGTCTTTTCAGCGGAGCGGTCCCGAGGGGAGCCCGGGCCACTG 156
QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 157 TGTACGGAGTTGGACCTTTGGGCGACTTGAACCTGCTGTGGGAGGCTCTTGGGGAC 216
QY 61 GlyAlaProSerGlnLeuHisLeuGlnSerGlnLysTyr-ArgSerAsnLysThrGlnTh 80
Db 217 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTATGAAG- 259
QY 80 rValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSe 100
Db 259 ----- 259
QY 100 rAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVa 120
Db 259 ----- 259
QY 120 lAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSe 140
Db 260 -----CCAAACGCCCGCGCTGGGCGCTCGAGCTGGACTTTTC 297
QY 140 rGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisly 160
Db 298 CGAGGATGACCCCTCGAGGCCACTGTCCATTTGGGCCCCACCTACATGGCCATCTCAT 357
QY 160 sValLeuileCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGl 180
Db 358 AGTTCTGATCTGCCAGTTCCACTACCGAAGTGTACAGAGGGCGGCTGGACCTGTGGA 417
QY 180 uProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaTh 200
Db 418 ACCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAAAGATTTGGAGCTAG 477
QY 200 rGlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTr 220
Db 478 TGGCTACAAGTGTATGGCGCTGCCGATGGNAAAGAGAGGATTTGTGGGCGAGTG 537
QY 220 pSerProileLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGl 240
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QY 240 yAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPr 260
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QY 300 aValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAl 320
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QY 600 rGlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProTh 620
Db 1678 CCAGCCCGCCAGGCGCCCGCCCTGACTCTGGGTATGAGAAGCACTTCTCTGCCAC 1737
QY 620 rProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1738 ACTGAGGAGCTGGGCGCTTCTGGGGCCCCCAGGCCACAGGTTCTTGCC 1786

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Search completed: February 23, 2005, 05:20:05  
Job time : 987 secs

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; LENGTH: 2663 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 139...2049  
 ; US-08-653-740-4

## Alignment Scores:

Pred. No.: 1,15E-270 Length: 2663  
 Score: 3498.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-088-950A-1 (1-636) x US-08-653-740-4 (1-2663)

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Db 1999 CCTGAGGAGTGCGGCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTGGCC 2046

# RESULT 2

US-09-073-594-4  
; Sequence 4, Application US/09073594  
; Patent No. 5925735  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sorecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,594  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2663 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 139..2049  
US-09-073-594-4

Alignment Scores:  
Pred. No.: 1,15e-270 Length: 2663  
Score: 3498.00 Matches: 636  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-088-950A-1 (1-636) x US-09-073-594-4 (1-2663)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
Db 139 ATGGGGGAGGAGCGGGCGCCCTTCTGGGCTGTGGCGCTGCCCAAGCTGGCGCTGCTG 198  
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Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
Db 379 GTGGCAGTGGCAGCGCGAGCGAGCTGGGTGGCCATTCTCTCGGGAACAGCTCACCATGTCT 438  
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120  
Db 439 GACAAACTCCTTGTCTGGGGCACTAAGACAGCGCCAGCCTCTCTGGCCCCCGCTCTCGTG 498  
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
Db 499 AACCTAGAAACCCCAATGAAGCAACGCCCGCTGGGCGCTTGAGCTGAGACTTTTCC 558  
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
Db 559 GAGGATGACCCCTGGAGGCCACTGTCCATTGGGCCCCACCTACATGAGCCATCTCATAAA 618  
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Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
Db 679 CCGAGCTGAAGACCATACCCCTGACCCCTCTTGAGATCCAAGATTTTGGAGCTAGCCACT 738  
Qy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220  
Db 739 GGCTACAAAGTGTATGGCCGCTGCCGAGTGGAGAAAGAGAGGATTTGTGGGGCGAGTGG 798  
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
Db 799 AGCCCCATTTTGTCTTCCAGACACCGCCTTCTCTCCAAAGATGTGTGGGTATCAGGG 858  
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
Db 859 AACCTCTGTGGGACGCTTGGAGGAGAGAACTTTTGTCTTATGAGAGCCCGGAGGGGCC 918  
Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
Db 919 TGTGTGAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTCTGAGCTCAGTCCAGAA 978  
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
Db 979 GGAATTACCTGCTGCTGCTCCCTAATCCAGTGGGCGAGTGGGCGCAGGCTGTCCGCT 1038  
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
Db 1039 GTCAACGCCCAAGCTGGGAGCCCTCTCAACACCTCTCTTTGGTCTGCTTGATTCAGCC 1098  
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
Db 1099 TCTGCCCCCGTAGCTGGCAGTCCAGAGCATCTCGTGGGAGCACGGAGCTACTGGTGACC 1158  
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
Db 1159 TGGCAACCGGGCGCTGGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGGAC 1218  
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
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Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
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Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
Db 1339 TTGGCCCTCTGCATCCTCCGCTCGGGGTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA 1398  
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
Db 1399 ACGCTTTGGGAGCTCCAAAGATGCCCTCCAGGGACCCCGCCCATAGCGTGGGGAGAGGTC 1458

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501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
1639 GGTCCCATCTCCGGCTTATCTACACAGATAACACCTGAGGTGGAAGTTCGCCAGGC 1698  
521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
1699 ATCTATTCTTGTGGGCTTGTTCCTGTTGGGTGTGGCTGAGCTGGCCACCTCTGGA 1758  
541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGlnLysValProAsp 560  
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561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
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581 GlyAspLeuProIleLeuGluValGluMetGluProProValMetGluSerSer 600  
1879 GGGGACTTGGCCATCTCGAAGTGGAGGAGATGGAGCCCCCGCGGTATGAGTCTCTCC 1938  
601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGlnLysHisPheLeuProThr 620  
1939 CAGCCCGCCAGGCCACCGCCGCTGTGATCTGGGTATGAGAAGCACTTCTCTGCCACA 1998  
621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
1999 CTTGAGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2046

## RESULT 3

US-09-275-925-4  
; Sequence 4, Application US/09275925  
; Patent No. 6080406  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/275,925  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E.  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673

TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2663 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 139..2049  
; US-09-275-925-4  
Alignment Scores:  
Pred. No.: 1.15e-270 Length: 2663  
Score: 3498.00 Matches: 636  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-088-950A-1 (1-636) x US-09-275-925-4 (1-2663)  
QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
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QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
Db 199 CCTCTGTTGTGGGTGCTTTTCCAGCGGAGCGCTCCAGGCGAGCGCGGCACTGCAG 258  
QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60  
Db 259 TGCTACGGAGTTGGACCTTGGGCGACTTGAATGCTGCTGGGAGGCTCTTGGGACCTG 318  
QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
Db 319 GGAGCCCCCTCCGAGTACACCTCCAGAGCCAAAGTACCGTTCCACAAAACCCAGACT 378  
QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
Db 379 GTGGCAGTGGCAGCGGAGCGAGCTGGGTGGCCATTCTCTCGGGAACAGCTCACCATGTCT 438  
QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
Db 439 GACAAACTCTTGTCTGGGGCACTTAAGGAGCGCCAGCCTCTCTGGCCCCCCTCTCTG 498  
QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
Db 499 AACCTAGAAACCCAAATGAAGCCAAAGCCCGCCCGCTGGGCGCTGACGTGGACTTTTCC 558  
QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
Db 559 GAGGATGACCCCTGGAGGCCACTGTCCATTGGGCCCCACCTACATGGCCATCTCATAAA 618  
QY 161 ValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
Db 619 GTTCTGATCTGCAGTTCACCTACCGAAGATGTAGAGGGCGGCTTGGACCTGCTGGAA 678  
QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
Db 679 CCGGAGCTGAAGACCATACCCCTGACCTTGTAGATCCAAGATTGGAGCTAGCCACT 738  
QY 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220  
Db 739 GGCTACAAAGTGTATGGCGGCTGCGCGATGGAGAAGAGAGATTTGGGGCGGAGTGG 798  
QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
Db 799 AGCCCCATTTTGTCTTCCAGACACCGCTTCTGTCTCCAAAAGATGTGGGTATCAGGG 858  
QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260



Db 859 AACCTCTGTGGAGCGCTGGAGGAGGAACCTTTGCTTCTATGGAAGGCCCGCCAGGGCCC 918  
Qy 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
Db 919 TGTGTGACAGGTGAGCTACAAAGTCTGTGTTCTGGGTGGAGGTCTGTGAGTCCAGAA 978  
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
Db 979 GGAATTAACCTGCTGCTGCTCCCTAATTCCTAGTGGGCGGAGTGGGCGAGGGTCTCGCT 1038  
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
Db 1039 GTCAACGCCACAGCTGGAGCCCTCTACCAACCTCTCTTTGGTCTGCTTGGATTCAGCC 1098  
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuValThr 340  
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Db 1159 TGGCAACCGGGCGCTGGGGAACCACTGGAGCATGTAGTGAGCTGGGCTCGAGATGGGAC 1218  
Qy 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyValAsnLeuSerAlaLeuPro 380  
Db 1219 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTCGGAACTCAGTGTCTCTTTACCA 1278  
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
Db 1279 GGGAAATTCACTGTCGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1338  
Qy 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
Db 1339 TTGGCCTCTGCATCTCGCTCGGGGTTCAGGAGGAATTAGCACCCCTAGTGGGGCCA 1398  
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
Db 1399 ACGTTTGGGCACTCCCAAGATGCCCTCCAGAGACCCCGCCATAGCGTGGGGAGAGTC 1458  
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460  
Db 1459 CCAAGCACCGAGCTTCGAGGCCACCTCACCACTACACCTTGTGTGCACAGATGGAAAC 1518  
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
Db 1519 AGCCCTCTCGTCTGCATGAATGTAGTGGAACACACAGAGTGTACCTCGCTCGCTGACCTT 1578  
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
Db 1579 CTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCT 1638  
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
Db 1639 GGTCCCATCTCCGGCTTCATCTACCAAGATAACACCTGAGTGGAAAGTTCTGCCAGGC 1698  
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
Db 1699 ATCCTATTCTTGTGGGCTGTGTTCTCTGTGGGTGGCTGAGCCTGGCCACCTCTGGA 1758  
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
Db 1759 AGGTGCTTACCACCTTAAGGCACAAAGTCTCGCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1818  
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
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Db 1879 GGGACTTGGCCATCTCTGGAAGTGGAGAGATGAGAGCCCGCCCGCGGTTATGAGTCTCTCC 1938  
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
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Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
Db 1999 CCTGAGGAGCTGGGCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTTGCC 2046

## RESULT 4

US-08-653-740-2  
; Sequence 2, Application US/08653740  
; Patent NO. 5792850  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2368 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 23..1759  
; US-08-653-740-2

Alignment Scores:  
Pred. No.: 7,92e-243 Length: 2368  
Score: 3150.00 Matches: 578  
Percent Similarity: 90.88% Conservative: 0  
Best Local Similarity: 90.88% Mismatches: 0  
Query Match: 90.05% Indels: 58  
DB: 1 Gaps: 1

US-10-088-950A-1 (1-636) x US-08-653-740-2 (1-2368)

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281 GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
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321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuValThr 340  
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421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440

203 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAAACAAACCCAGACT 262  
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263 GTGGCAGTGGCAGCCGAGCGAGCTGGGTGGCCATTCTCTCGGGAAACAGCTCACCATGTCT 322  
101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
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141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
443 GAGGATGACCCCTGGAGGCCACTGTGTCATTGGGCCCCACCTACATGGCCATCTCATAA 502  
161 ValLeuLeuLeuLeuPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
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181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
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221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
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241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
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301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
923 GTCAACGCCACAAAGCTGGGAGCTCTCACCAACCTCTCTTTGGTCTGCTTGGATTACGCC 982  
321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuValThr 340  
983 TCTGCCCCCTGAGCTGGCAGTCAAGCAGATCGCTGGGAGCAGCGAGTACTGTGTGACC 1042  
341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
1043 TGGCAACCGGGGCTGGGGAACCATGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1102  
361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
1103 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTGGGAACCTCAGTGTCTGTATTACCA 1162  
381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
1163 GGAATTTTCACTGTCCGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1222  
401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
1223 TTGGCCCTCTGCATCTCTCCGTCTGGGGGTTTCAGGGAGGAATTAGACCCCTAGTGGGCCA 1282  
421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440

1283 AGCTTTGGGACTCCAAAGATGCCCTCCAGGGACCCCGCCATAGCGTGGGGAGAGTCT 1342  
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1343 CCAAGGCCACAGCTTCGAGGGCCACCTCACCCACATACACCTTGTGTGTCACAGAGTGAACC 1402  
461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
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1463 CTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGAGGCCCTCTCT 1522  
501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
1523 GGTCCCATCTCCCGGCTTCATCTACAGATAACACCTGAGGTGGAAGTTCTGCGCGGC 1582  
521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
1583 ATCTATTCTTGTGGGGCTTGTCTCTGTGGGGTGTGGCTGAGCTGGCCACCTCTCGA 1642  
541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
1643 AGGTGCTACCACTAAGGCACAAAGTACTGCCCGCTGGGTCTGGAGAGAAAGTTCTCTGAT 1702  
561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
1703 CTGCAACAGCAGTTCA----- 1720  
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601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
1720 ----- 1720  
621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
1721 -----GGCTTTCTGGGGCCCCCAGCCAGGTTCTGGCC 1756

## RESULT 5

US-09-073-594-2  
; Sequence 2, Application US/09073594  
; Patent No. 5925735  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,594  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648

REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6673

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2368 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 23...1759

US-09-073-594-2

#### Alignment Scores:

Pred. No.:	7.92e-243	Length:	2368
Score:	3150.00	Matches:	578
Percent Similarity:	90.88%	Conservative:	0
Best Local Similarity:	90.88%	Mismatches:	0
Query Match:	90.05%	Indels:	58
DB:	2	Gaps:	1

US-10-088-950A-1 (1-636) x US-09-073-594-2 (1-2368)

Qy	1	MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu	20
Db	23	ATGGGGGAGGACGGGGCCCTTTCTGGGTGTGGCGCTGCCAAGCTGGCGCTGCTG	82
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlnGlySerAlaGlyProLeuGln	40
Db	83	CCTCTGTGTGGTGTCTTTCACGGGACGGCGTCCCCAGGGGACGGCGGCGCCACTGCAG	142
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	143	TGCTACGGAGTTGACCCCTTGGGGGACTTGAACCTGCTCGTGGGAGCCTCTTGGGGACCTG	202
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	203	GGAGCCCTCCGAGTTACCTTCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT	262
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer	100
Db	263	GTGGCAGTGGCAGCGGAGGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGTCT	322
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
Db	323	GACAAACTCCTTGTCTGGGGCAGCTAAGGCAGGCCAGCCCTCTCTGGCCCCCGCTTCGTG	382
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	383	AACCTAGAAACCCAAATGAAGCCAAACGCCCGCTGGGCCCTGACGTGGACTTTTCC	442
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProTrpProSerHisLys	160
Db	443	GAGGATGACCCCTGGAGGACACTGTCCATTGGGCCCCACCTACATGCCATCTCATAAA	502
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaIleTrpThrLeuLeuGlu	180
Db	503	GTTCTGATCTGCCAGTTCCACATACCGAAGATGTCCAGGAGCGGCGCTGGACCTGCTGAA	562
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	563	CCGGAGCTGAAGACATACCCCTGACCCCTGTTGAGATCCAAAGATTTGGAGCTAGCCACT	622
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
Db	623	GGCTACAAAGTGTATGGCCGCTGCGGATGGAGAAAGAGAGGATTTGTGGGGCGAGTGG	682
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	683	AGCCCCATTTGTCTCCAGACACCGCCTTCTGCTCCAAAGAGATGTGGGTATCAGGG	742

Qy	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	743	AACCTCTGTGGAGCCCTGGAGGAGAGAACCTTTGTTCTATATGAGAGGCCCCAGGGCCC	802
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	803	TGTGTGCAAGGTGAGCTACAAAGTCTGTTCTGGGTTGGAGTCTGAGCTGAGTCCAGAA	862
Qy	281	GlyIleThrCysCysCysSerLeuIleProSerClyAlaGluTrpAlaAArgValSerAla	300
Db	863	GGAATTACCTGCTGCTCTCCCTAAATTCCAGTGGGGCGGAGTGGGCGAGGTTCCGCT	922
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	923	GTCAACGCCACAAGCTGGGAGCCCTCTACCAACCTCTCTTTGGTCTGCTGGATTACGCC	982
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
Db	983	TCTGCCCGCGTAGCGTGGCAGTCAAGCATCGCTGGGAGCAGGAGCTACTGCTGACC	1042
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaAArgAspGlyAsp	360
Db	1043	TGGCAACCGGGGCTGGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGGAC	1102
Qy	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
Db	1103	CCCTGGAGAAATCAACTGGGTCCGGCTTCCCTCCCTGGGAAACCTCAGTGTCTGTGTACCA	1162
Qy	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
Db	1163	GGGAATTTCACTCTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC	1222
Qy	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
Db	1223	TTGGCCTCTGCATCTCTCGTCTGGGGTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA	1282
Qy	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
Db	1283	ACGCTTTGGGCACTCCAGATGCCCCCTCCAGAGACCCCCCCCATAGCGTGGGAGAGGTC	1342
Qy	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
Db	1343	CCAAGGCACCGCTTCAGGCCACCTCACCCATACACCTTGTGTGCACAGAGTGGAAACC	1402
Qy	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
Db	1403	AGCCCCCTCGTCTGCATGAATGTGAGTGGCAACACACAGAGTGTCAACCTGCTGACCTT	1462
Qy	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
Db	1463	CCTTGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCTCT	1522
Qy	501	GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly	520
Db	1523	GGTCCCATCTCCGGCTTCATCTACACAGATAACACCTGAGGTGGAAAGTTCTGCCGGGC	1582
Qy	521	IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
Db	1583	ATCCTATTCTGTGGGGCTTGTTCCTGTGGGGTGTGGCCTGAGCCTGGCCACCTCTGGA	1642
Qy	541	ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp	560
Db	1643	AGGTGCTACCACTTAAGGCACAAGTACTGCCCCGCTGGGTCTGGGAGAAAGTTCTTGAT	1702
Qy	561	ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu	580
Db	1703	CTTGCCCAACAGCAGATTCA-----	1720
Qy	581	GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer	600
Db	1720	-----	1720

QY 601 GinProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
Db 1720 ----- 1720  
QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
Db 1721 -----GGCCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 1756

## RESULT 6

US-09-275-925-2  
; Sequence 2, Application US/09275925  
; Patent No. 6080406  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/275,925  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2368 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 23..1759  
US-09-275-925-2

Alignment Scores:  
Pred. No.: 7,92e-243 Length: 2368  
Score: 3150.00 Matches: 578  
Percent Similarity: 90.88% Conservative: 0  
Best Local Similarity: 90.88% Mismatches: 0  
Query Match: 90.05% Indels: 58  
DB: 3 Gaps: 1

US-10-088-950A-1 (1-636) x US-09-275-925-2 (1-2368)

QY 1 MetArgGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
Db 23 ATGCGGGAGGCGAGGGGCGCCCTTCTGGCTGTGGCGCTGCCAAGCTGGCGCTGCTG 82  
QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
Db 83 CCTCTGTGTGGGTGCTTTTTCACGGAGCGCGTCCCGAGGAGCGCCCGGCGACCTGCG 142  
QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 143 TGCTACGGAGTTGGACCTTGGGCGACTTGAACCTGCTGGGAGCCTCTTGGGAGCCTG 202  
QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
Db 203 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAAACAAAACCCAGACT 262  
QY 81 ValAlaValAlaAlaGlyValArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
Db 263 GTGGCAGTGGCAGCGCGAGCGAGCTGGGTGGCCATTCTCTCGGAAACAGCTCACCATGTCT 322  
QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120  
Db 323 GACAAACTCTTGTCTGGGGCACTAAGGCAGGCCAGCCTCTCTGGCCCCCGCTCTCGTG 382  
QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
Db 383 AACCTAGAACCCAAATGAAGCCAAACGCCCGCGCTGGGCCCTGAGGTGAGCTTTTCC 442  
QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
Db 443 GAGGATGACCCCTGGAGGCCACTGTCCATTGGGCCCCCACCCTACATGCCCATCTCATAAA 502  
QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
Db 503 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTGAGAGCGGCCCTGGACCTGCTGGAA 562  
QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
Db 563 CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTAGATCCCAAGATTTGGAGTAGCCACT 622  
QY 201 GlyTyrLysValTyrGlyValArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220  
Db 623 GGCTACAAAGTGTATGGCGCGTGCAGATGAGAAAGAGAGGATTCTGGGGCGAGTGG 682  
QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
Db 683 AGCCCATTTTGTCTTCCAGACACCGCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG 742  
QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
Db 743 AACCTCTGTGGAGCGCTGGAGGAGGAGAACCTTTGCTTATGGAAGCCGCCAGGGGCC 802  
QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
Db 803 TGTGTGCAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGTCTGGAGTCTGAGTCCAGAA 862  
QY 281 GlyIleThrCysCysSerIleuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
Db 863 GGAATTACCTGCTGCTCTCCCTAATTCCTCAGTGGGGCGAGTGGGGCCAGGGTGTCCGCT 922  
QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
Db 923 GTCAACGCCCAAGCTGGGAGCCTCTCACCAACCTCTCTTTGGTCTGCTTGAATTACGCC 982  
QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
Db 983 TCTGCCCCCGCTAGCGTGGCAGTCAAGCAGCAGTCTGGGAGCAGCAGCTACTGTTGACC 1042  
QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
Db 1043 TGGCAACCGGGGCGCTGGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1102  
QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
Db 1103 CCCCTGGAGAAACTCAACTGGGTCCGGTTCCTCCCTGGGAACTCAGTGTCTGTATACA 1162  
QY 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
Db 1163 GGGAAATTTCACTGTGGGGTCCCTTATCGAATCACTGTGACCGCAGTCTCTGCTTCAGGC 1222  
QY 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420



QY	234	LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGlulProLeuLeu	253
Db	692	GAAGATGTGGTATCTCGGGACCGCTGTGAACAACCTTCGGCAAAACGGGCAGCCCTGCT	751
QY	254	LeuTrpLysAlaProGlyProCysValGlnValSerTyrlsValTrpPheTrpValGly	273
Db	752	GTCCTGGGAAGACCACCAAGACTTGTTGCAGGTGACTTACACAGTCTCGTTTGGGGCTGGGA	811
QY	274	GlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuLeuLeuProSerGlyAla	293
Db	812	GATATTACTACACTCAAGAAGAGGTCCCGTCTGCAAGTCCCCTGTCCTGCATGATG	871
QY	294	GluTrpAlaArgValSerAlaValAsnAlaThrserTrpGluProLeuThrAsenLeuSer	313
Db	872	GAGTGGGCTGTGGTCTCTCTCGGCCAACAGCACAGCTGAGTGGTGGCTCCACCAACCTGTCT	931
QY	314	LeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerlleAlaGly	333
Db	932	CTGGTGTGCTTGGCTCCAGAACTGCCCCCTGTGAOCTGGAGGTGACAGTGTGTAGTGGG	991
QY	334	SerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHisValVal	353
Db	992	AGCCCGGGATAAAGGTGACTCGGAACAAGGACNACAGGAACCATTTGGAGTATGTGGT	1051
QY	354	AspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGly	373
Db	1052	GACTGGGCTCAAGATGTGTGACAGCTGGACAAGCTCAACTGAGCCGCTCTCCCCCTCGGA	1111
QY	374	AsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrrArgIleThrVal	393
Db	1112	AACCTCAGCACATTGTTTACCAGGGGAGTCTCAAAGGAGGGGTACCTATCGAATTTACAGT	1171
QY	394	ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerSerValTrpGlyPheArgGluGlu	413
Db	1172	ACTGCAGTATACTCTGGAGGATTAGCTGTCTGCACCTCAGTTTGGGGATTTCAGAGAGAG	1231
QY	414	LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro	433
Db	1232	TTAGTACCCCTTGCTGGGCCAGCAGTGTGGCACTTCCAGATGACCCCCCAGGGACACCT	1291
QY	434	AlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrrThr	453
Db	1292	GTTGTAGCCCTGGGGAGAAGTACCAAGACACACAGCTCAGAGGCCAGGCTACTCACTACAC	1351
QY	454	LeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGln	473
Db	1352	TTCGCGATACAGACAGCAGAGCCCTCTCCACTGTCTGCAGGAACGTGACGACTCAACCCAG	1411
QY	474	SerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThr	493
Db	1412	ACTGCCACTCTGCCCAACCTTCACTCGGGTTCCTTCAAGCTGTGGGTGACGGTGTCCACC	1471
QY	494	IleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeu	513
Db	1472	GTTGCAGACAGGGGCCACCCTGTGTCCGCACTTTCACCTTCCACCTACAGATAATAGGATC	1531
QY	514	ArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuGlyCysGly	533
Db	1532	AGGTGGAAAAGCTCTGCCCCCTGGTTCTTCTCCCTGTGGGGTTTTGCTTCGTAGGGCTGTGGC	1591
QY	534	LeuSerLeuAlaThrSer-----GlyArgCysTyrrHisLeuArgHisLysVal	549
Db	1592	CTGAGCTGGCCAGTACCAGGTGCCTACAGGCCAGGTGTCTTACACTGGCGACACAGTTG	1651
QY	550	LeuProArgTrpTrpTrpGluLysValProAspProAlaAsnSerSerGlyGlnPro	569
Db	1652	CTTCCCCAGTGGATCTGGGAGAGGGTTCTCTGATCTCTGCCAACAGCAATTTCTGGGCAACCT	1711
QY	570	HisMetcluglnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGlu	589
Db	1712	TACATCAAGGGGTGAGCCCTGCCCAACCCCAAGGACCGACCAATCTCTGGAGGTGGAG	1771
QY	590	GluMetGluProProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu	609

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Db      1772 GAAGTGGAGCTACAGCCTGTTGTGGAGTCC-----CCTAAGCCTCTGCCCGGATT 1822
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Qy      610 AspSerGlyTyrGluLysHisPheLeuProThrProGluGluLeuGlyLeuLeu 627
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Db      1823 TACTCTGGGTATGAGAAACAATCTTCTCTGCCACACAGAGGAGCTGGCCCTTCTA 1876
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RESULT 8
US-09-073-594-6
; Sequence 6, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1882
US-09-073-594-6

Alignment Scores:
Pred. No.: 4,66e-154 Length: 2589
Score: 2044.00 Matches: 388
Percent Similarity: 72.65% Conservative: 61
Best Local Similarity: 62.78% Mismatches: 161
Query Match: 58.43% Indels: 8
DB: 2 Gaps: 3

US-10-088-950A-1 (1-636) x US-09-073-594-6 (1-2589)

Qy      14 LeuProLysLeuAlaLeuLeuProLeuLeuTrrValLeuPheGlnArgThrArgProGln 33
          ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::|||
Db      35 CTCACGCGGTGGAGCTTCTGTCTGCTGATGTCGCTGCTCGGGACGCGGCCCCAC 94
          ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::|||
Qy      34 GlySerAlaGlyProLeuGlnCysTyrGlyValGlyProLeuGlyAspLeuAenCysSer 53
          ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::|||
Db      95 GGCAGTCCAGGCCCATGTGCAGTGTCTAAGGTCGGTCCCTCGGGAATCTCTGAATGCTCC 154
          ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::||| ||:::|||
Qy      54 TrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyr 73
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Db 155 TGGGAACCTTTGGGGGAGCTCCAGACTCCAGCTGTGCTGTATACAGAGTCAGAAATAC 214  
Qy 74 ArgSerAsnLysThrGlnThrValAlaValAlaAlaGlyArgSerTrpValAlaIlePro 93  
Db 215 CATCCATAGAGTCTGGGAGGTGAAGTCTTCCAAACAGAGTTGGTGACCATTC 274  
Qy 94 ArgGluGlnLeuThrMetSerAspLysLeuValTrpGlyThrLysAlaGlyGlnPro 113  
Db 275 CGGAACAGTTTCACCATGGCTGCACAACTCTCATCTGGGGGACACAAAGGAGCGCT 334  
Qy 114 LeuTrpProValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeu 133  
Db 335 CTGTGGCTCTGTCTGTGAACCTGGAGACCCAAATGAAGCCAGACACCTCAGATC 394  
Qy 134 GlyProAspValAspPheSerGluAspProLeuGluAlaThrValHisTrpAlaPro 153  
Db 395 TTCTCTCAAGTGGATATTCTTGAGAGCAACCTGGAGGCCACTGTGCAGTGGGCGCG 454  
Qy 154 ProThrTrpProSerHisLysValLeuIleCysGlnPheHisTyrArgCysGlnGlu 173  
Db 455 CCGGTGTGGCCACCGCAGAAAGCTCTCACCTGTCTCAGTTCCGGTACAAAGGAATGCCAGCT 514  
Qy 174 AlaAlaTrpThrLeuGluProGluLeuLysThrIleProLeuThrProValGluIle 193  
Db 515 GAAGCATGGACCCGGCTGGAGCCCGAGCTGAAGACAGATGGGCTGACTCTCTGTGTGAGATG 574  
Qy 194 GlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213  
Db 575 CAGAACCTGGAACTGGCACCTGTACCAGGTGTCTGGCCGCTGCCAGGTGGAGACCGA 634  
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaPro 233  
Db 635 TATCCA--TGGGGCGAGTGGAGTTCGCCCTGTCTCCAGAGCCCATCTTAGATCT 691  
Qy 234 LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeu 253  
Db 692 GAAGATGTGGGTATCGGGACCGCTCTGTGAACCTTCTGGCAACCGGCGAGCCCTGCTT 751  
Qy 254 LeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrpValGly 273  
Db 752 GTCTGGAAGGACCCAGACCTTGTGTGAGTGACTTACACAGTCTGTGTTGGGGTGA 811  
Qy 274 GlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIleProSerGlyAla 293  
Db 812 GATATTACTACACTCAAGAGAGGTCCGCTGCTGCAAGTCCCTGTCTGCAATGATG 871  
Qy 294 GluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAsnLeuSer 313  
Db 872 GAGTGGGCTGGGTCTCTCTGGCAACAGCAGCAGCTGGGTGGCTCCCAACCACTGTCT 931  
Qy 314 LeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerIleAlaGly 333  
Db 932 CTGTGTGTCTGGCTCCAGATCTGCCCTGTGACGTGGGAGTGACAGTGTGTATGGG 991  
Qy 334 SerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGluHisValVal 353  
Db 992 AGCCGAGGATAAAGGTGACCTGGAACAAGGACCAGGAAACCATTTGGAGTATGTGTG 1051  
Qy 354 AspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGly 373  
Db 1052 GACTGGGCTCAAGATGTGACAGCTGGCAAGCTCAACTGGACCCGCTCTCCCCCTGGA 1111  
Qy 374 AsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVal 393  
Db 1112 AACCTCAGCATTTGTACAGGGGAGTTCAAGAGGGGTACCTATCGAATTACAGTG 1171  
Qy 394 ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluGlu 413  
Db 1172 ACTCAGTATCTCTGGAGGATTAGTCTGCACCTCCAGTTCAGTTGGGATTACAGAGGAG 1231  
Qy 414 LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro 433  
Db 1232 TTAGTACCCCTTGTGGGCCAGCAGTGTGGCGACTTCCAGATGTACCCCGGAGACACCT 1291

Qy 434 AlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrThr 453  
Db 1292 GTTGTAGCTGGGAGAGTACCAAGACACAGCTCAGAGCCAGGCTACTCTACTACACC 1351  
Qy 454 LeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGln 473  
Db 1352 TTCTGCATACAGACGAGAGCCCTCTCCACTGTCTGCAGGAACGTCGAGCAGTCAACCCAG 1411  
Qy 474 SerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThr 493  
Db 1412 ACTGCCACTCTGCCAACCTTCTACTCGGGTTCCTTCAAGCTGTGGGTGAGCGTGTCCACC 1471  
Qy 494 IleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeu 513  
Db 1472 GTTCAGGACAGGGCCACCTGGTCCGACCTTTCACCTTCCACCTACCCAGATAATAGATC 1531  
Qy 514 ArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGly 533  
Db 1532 AGGTGGAAGCTCTGCCCTGTCTTCTGTCCTGTGGGTTTGTCTTGTATGGGCTGTGGC 1591  
Qy 534 LeuSerLeuAlaThrSer-----GlyArgCysTyrHisLeuArgHisLysVal 549  
Db 1592 CTGAGCTGGCCAGTACCAGGTGCTTACAGCCAGGTGCTTACCTGGCCAGACAAGTTG 1651  
Qy 550 LeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerSerGlyGlnPro 569  
Db 1652 CTTCCCGAGTGGATCTGGGAGAGGTTCTCTGATCCTGCCAACAGCAATTCCTGGCAACCT 1711  
Qy 570 HisMetGluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGlu 589  
Db 1712 TACATCAAGGAGGTGAGCTGCCCAACCGCCCAAGACGAGCCATCTCTGGAGTGGAG 1771  
Qy 590 GluMetGluProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu 609  
Db 1772 GAAGTGGAGTACAGCTGTGTGGAGTGC-----CTTAAGCTCTGCCCGCAT 1822  
Qy 610 AspSerGlyTyrGluLysHisPheLeuProThrProGluLeuGlyLeuLeu 627  
Db 1823 TACTCTGGGTATGAGAAACACTTCTCTGCCACACAGAGGAGCTGGGCTTCTA 1876

## RESULT 9

US-09-275-925-6  
; Sequence 6, Application US/09275925  
; Patent No. 6080406  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/275,925  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:



Db 1823 TACTCTGGTATGAGAAACACTTCTGCCCCACACAGAGGAGCTGGGCTTCTTA 1876

RESULT 10  
US-08-685-118-1  
; Sequence 1, Application US/08685118  
; Patent No. 5840530  
; GENERAL INFORMATION:  
; APPLICANT: Gubler, Ulrich A  
; APPLICANT: Presky, David H  
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,118  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silverman, Robert A.  
; REGISTRATION NUMBER: 35,682  
; REFERENCE/DOCKET NUMBER: CD 9195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 235-2863  
; TELEFAX: (201) 235-2363  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4040 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 641..3226  
US-08-685-118-1

Alignment Scores:  
Pred. No.: 2.02e-20 Length: 4040  
Score: 381.50 Matches: 189  
Percent Similarity: 38.18% Conservative: 92  
Best Local Similarity: 25.68% Mismatches: 285  
Query Match: 10.91% Indels: 172  
DB: 2 Gaps: 35

US-10-088-950A-1 (1-636) x US-08-685-118-1 (1-4040)

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Qy 27 ----- 27

Db 943 CAACACTGGCTGTATCAATAGTAGTAATCAATATGTCGAGCAGAGATCTTCGTGG 1002

Qy 28 ----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyrGlyValGlyPr 46  
Db 1003 TGTGCTCCAGACAGCCTCAAAAT-----TTATCCTGCATACAGAGGGAGA 1050

Qy 46 oLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp----- 59  
Db 1051 ACAGGGAGACTGTGGCCTGCACCTCGGAAAGAGGACGACACACCCACTTATACACTGAGTA 1110

Qy 60 -----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln----- 71  
Db 1111 TACTCTACAGCTAAGTCGACCAAAATTTAACTCTGGCAGAGCAATGTAAAGACATTTA 1170

Qy 72 -----LysTyrArgSerAsnLysTh 78  
Db 1171 TTGTGACTATTGTGACTTTTGGAAATCAACCTCACCCCTGAATCACCTGAATTTTCCAC 1230

Qy 78 xGlnThrVal---AlaValAlaAlaGlyArgSerTrpValAlaLeProArgGluGlnLe 97  
Db 1231 AGCCAAGTTACTCTGTCAATAGTCTTGAAGCTCTCTTCACTTCA---TCCACATT 1287

Qy 97 uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr 117  
Db 1288 CACATTCTTGGACATAGTG-----AGGCTCTT---CCTCC 1320

Qy 117 oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa 137  
Db 1321 GTGGACATTAGAAATCAAAATTTCAA---AAGGCTTCCTGAGCAGA----- 1363

Qy 137 lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr 157  
Db 1364 -----TGTACCCCTTTATTGGAGA-----GA 1383

Qy 157 oSerHisLysValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpTh 177  
Db 1384 TGAGGGACTGTACTGTCTTAATCGACTCAGATATCGCCCGCCAGTAACAGCGGCTCTGGAA 1443

Qy 177 xLeuLeuGluProGluLeuLysThrIleProLeuThrProVal-----GluIl 193  
Db 1444 TATG-----GTTAATGTTTACAAAGGCCCAAGAGACACATGATT, 1482

Qy 193 eGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGl 213  
Db 1483 GCTGGATCTGAAACCATTTACAGAAATATGAATTCAGATTCTCTCAAGCTACATCTTTA 1542

Qy 213 uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro-----Pr 230  
Db 1543 TAAGGGAGTGTGGAGTGTGAGTGAATCATTTGAGAGCACAACACACAGAGAGAGGCC 1602

Qy 230 oSerAlaProLysAspValTrpValSerGlyAsnLeuLysGlyThrProGlyGlyGluGl 250  
Db 1603 TACTGGGATGTTAGATGCTGTGATGAAACCGCACATTTGACTAC---AGTAGACAACA 1659

Qy 250 uProLeuLeuTrpLys-----AlaProGlyProCysValGlnVa 264  
Db 1660 GATTTCTCTTTCTGGAGAAATCTGAGTGTCTCAGAGGCAAGAGGAAAAATTTCTCCACTA 1719

Qy 264 lSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu-----GlyIl 282  
Db 1720 TCAGGTGACCTTGCAGGAGCTGACAGGAGGAGGAAAGCCATCACACAGAACATCACAGACA 1779

Qy 282 eThrCysCysSerLeuIleProSerGlyAlaGluTrpAla---ArgValSerAlaVa 301  
Db 1780 CACCTCTCGACACACAGTCATCTCTAGAACCGGAAATTTGGCTGTGGCTGTCTGTCGAGC 1839

Qy 301 lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe 319  
Db 1840 AAATTTCAAAAGGAGTCTCTGCCACTCGTATTAAACATAATGAACCTGTGTGAGGAGG 1899

Qy 319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa 339  
Db 1900 GTTGTGCTCTCTCGCAGGCTCTCTGCAAACTCA---GAGGGCATGGACACACATCTTGGT 1956

Qy 339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl 356  
Db 1957 GACTTGGACGCTCCCGAGGAAAGATCCCTCTGTGTTTTCAGGAGTACGTGTGGAATGGAG 2016

Qy 356 aaArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGl 373  
Db 2017 AGAGCTCCATCCAGGGGGTGACACACAGAGTCCCTCTTAAACTGCTACGGAGTGACCCCTA 2076



Qy	97	uThrMetSerAspIysLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr	117
Db	1288	CACATCTTGGACATAGTG-:::     :::     :::	1320
Qy	117	oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa	137
Db	1321	GTGGGACATTAGATCAAAATTCAA--AAGGCTTCGTGAGCAGA-----	1363
Qy	137	lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr	157
Db	1364	-----TGTAACCCTTTATTGGAGA-----GA1383	
Qy	157	oSerHisLysValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaTrpTh	177
Db	1384	TGAGGGACTGTGCTACTGCTTAATCCACATAGATATCGGCCCATTAACAGCAGGCTCTGGA	1443
Qy	177	rLeuLeuGluProGluLeuLysThrIleProLeuThrProVal-----GluIl	193
Db	1444	TATG-----GTTAATGTTACAAGGCCAAAGGACACATGATTT1482	
Qy	193	eGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGl	213
Db	1483	GCTGGATCTGAACCAATTTACAGAAATATGAATTTTCAGATTTCCCTTAAGCTACATCTTTA	1542
Qy	213	uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro-----Pr	230
Db	1543	TAAGGGAAGTTGGAGTGATTTGAGTGGAATCATTCAGAGCACAACACCCAGGAAGAGACC	1602
Qy	230	oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGl	250
Db	1603	TACTGGGATGTTAGATGCTGTTACATGAACCGGCACATTGACTAC---AGTAGACAACA	1659
Qy	250	uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa	264
Db	1660	GATTTCTCTTCTCGGAAGAAATCTGAGTGCTCAGAGGCAAGAGAAAATTTCTCCACTA	1719
Qy	264	lSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu-----GlyIl	282
Db	1720	TCAGGTGACCTTGCAGGAGCTGCAGAGGGAAGGCCATGACACAGAACATCATCAGACGA	1779
Qy	282	eThrCysCysSerLeuIleProSerGlyAlaGluTrpAla---ArgValSerAlaVa	301
Db	1780	CACCTCTGGACCCACAGCTCATCTCTAGAACCGGAATTTGGGCTGTGCTGTCTGTGAGC	1839
Qy	301	lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe	319
Db	1840	AAATTTCAAAGGAGTTCCTGCCCCACTCGTATTTAAACATATGAACCTGTGTGAGGCAGG	1899
Qy	319	rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa	339
Db	1900	GTTCGTGCTCTCCGACAGTCTCTGCAAACTCA--GAGGCGCATGGACAACATTTCTGGT	1956
Qy	339	lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl	356
Db	1957	GACTTGGACGCTCCACAGGAAGATCCCTCTGCTGTTTCAGGAGTACGTGTGGATGGAG	2016
Qy	356	aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProGl	373
Db	2017	AGAGCTCCATCCAGGGGGTGACACACAGGTCCTCTAAACTGGCTGCGGAGTCGACCTTA	2076
Qy	373	yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVa	393
Db	2077	CAATGTGTGCTCTGATTTTCAGAGAACAATAAAATCCTACATCTGTTATGAAATCCGTGT	2136
Qy	393	lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerSerValTrpGlyPheArgGluGl	413
Db	2137	GTATGCACTCTCAGGGGAT---CAAGGAGGATGCAGCTCCATCTCGGTAACTCTAAGCA	2193
Qy	413	uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr	433
Db	2194	CAAAAGCACCATGATGGCCCGCCCACTAATATGCAATCATCAGAG---GAAAAGGGGAGCAT	2250

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433 oAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisIleuLeuThrHisTyrTh 453
2251 TTTAAATTTTCAAGAACAGCATTTCCAGTCCAGGAGCAAAATGGCTGCTCTCTCATATATAG 2310
453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467
2311 GATATACTGGAGAGGAGGACTCCAACTCCAGCCTCAGCTCTGTGAAATTTCCCTACAG 2370
467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
2371 AGTCTCCAAAATTCACATCAATCAATAAAGCAGCTGCAG--CCCGAGTGACATATGTCCT 2427
487 uTrpValThrAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHi 507
2428 GTGATGACAGCTCTGACAGCTGCTGTGTGAAAGTTCCACGGAATGAGAGGGAATTTTG 2487
507 sLeuProAspAsnThr-LeuArgTrpLysValLeuPro-----GlyIleLeuPheL 524
2488 TCTCAAGGTAAAGCCAATTGGATGGCGTTTGTGGCAACCAAGCATTTGCAATTGCTATCAT 2547
524 euTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrH 544
2548 CATGCTGGGCATT-----TCTCAACGCATTACTTCCAGCAAAAGGTGTTGT 2595
544 isLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnS 564
2596 T-CTCTAGCAGCCCTCAGACCTCAGTGTGTAGCAGAGAAATTCAGATCCAGCAAATA 2654
564 erSerSerGlyGlnProHis-----MetGluGlnValProGluAlaGlnP 579
2655 GCATTCGGTAAAGAAATATCCCATTCAGAGAGAGAACACAGACTGCCCTTGGACAGGC 2714
579 roLeuGlyAspLeuProIleLeuGluValGluGluMetGluProPro----- 595
2715 TCTGTAGACTGGCCCAAGCCTGAA-----GATCTGAACCCCTGGTGCATCA 2762
596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu----- 609
2763 GTGAAGTCTCTCA-TCAAGTGACCCAGTTTTCAGACATCCCCCTGCTCCAAGTGCCCA 2821
610 -----AspSerGlyTyr-GluLysHisPheLeuProThrPro 621
2822 CAAGGGAAAAAGGAATCCAAGTGTCATCAGGCTCTTGAGAAAGACATGATGCACAGTGCC 2881
622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
2882 TCA-----AGCCCAACCACTCCAAGAGCTCTC 2908

RESULT 12
US-08-914-520-1
; Sequence 1, Application US/08914520
; Patent No. 5919903
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,520
; FILING DATE:
; CLASSIFICATION:

```

PRIOR APPLICATION DATA: 08/685,118  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silverman, Robert A.  
 REGISTRATION NUMBER: 35,682  
 REFERENCE/DOCKET NUMBER: CD 9195  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 235-2863  
 TELEFAX: (201) 235-2363  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4040 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 641..3226  
 US-08-914-520-1

Alignment Scores:  
 Pred. No.: 2,02e-20 Length: 4040  
 Score: 381.50 Matches: 189  
 Percent Similarity: 38.18% Conservative: 92  
 Best Local Similarity: 25.68% Mismatches: 285  
 Query Match: 10.91% Indels: 172  
 DB: 2 Gaps: 35

US-10-088-950A-1 (1-636) x US-08-914-520-1 (1-4040)

QY 12 TrpProLeuProLysLeuAla-Leu-----LeuProLeuLeuTrpValLeuPhe----- 27  
 DB 883 TGCCACTCCCTCAATTCTCAAGTCACAGCTCTCCCTTGGTACACCTTGTGTCTG 942  
 QY 27 ----- 27  
 DB 943 CAAACTGGCCTGATCAATAGTGAATTCAAATATGAGGAGAGAGATCTTCCTGG 1002  
 QY 28 ----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyxGlyValGlyPr 46  
 DB 1003 TGTTCCTCCAGACAGCTCAAAAT-----TTATCCTGCATACAGAGGAGA 1050  
 QY 46 oLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp----- 59  
 DB 1051 ACAGGGAGCTGTGGCTGCACCTGGGAAAGAGGAGCAGACACCCACTTATACACTGAGTA 1110  
 QY 60 -----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln----- 71  
 DB 1111 TACTCTACAGCTAGTGGACCAAAATTTTAACCTGGCAGAACATGTAAAGACATTTA 1170  
 QY 72 -----LysTyxArgSerAsnLysTh 78  
 DB 1171 TTGTGACTATTGGACTTTGGAATCAACCTCACCCCTGATCACTGAAATCCAAATTTTCC 1230  
 QY 78 rGlnThrVal---AlaValAlaAlaGlyArgSerTrpValAlaAlaProArgGluGlnLe 97  
 DB 1231 AGCCAAGGTACTGCTGCTCAATAGTCTTGGAGCTCTCTTCACTTCCA---TCCACATT 1287  
 QY 97 uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr 117  
 DB 1288 CACATTTCTTGACATATG-----AGGCCCTTT---CCTCC 1320  
 QY 117 oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa 137  
 DB 1321 GTGGGACATTAGATCAAAATTTCAA---AAGGCTTCGTCGAGCAGA----- 1363  
 QY 137 lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr 157  
 DB 1364 -----TGTAACCTTTATTGGAGA-----GA 1383

QY 157 oSerHisLysValLeuIleCysGlnPheHisTyxArgCysGlnGluAlaAlaTrpTh 177  
 DB 1384 TGAGGGAGCTGTACTGTCTTAATCACTCAGATATCGCCCAAGTAAACAGAGGCTCTGAA 1443  
 QY 177 rLeuLeuGluProGluLeuLysThrIleProLeuThrProVal-----GluIle 193  
 DB 1444 TATG-----GTTAATGTTTACAAAGGCCAAAGAACACATGATTT 1482  
 QY 193 eGlnAspLeuGluLeuAlaThrGlyTyxLysValTyxGlyArgCysArgMetGluLysG 213  
 DB 1483 GCTGGATCTGAACACATTACAGAAATATGAATTTTCAGATTTCTCTTAACTTACATCTTA 1542  
 QY 213 uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro-----Pr 230  
 DB 1543 TAAGGGAAGTTGGAGTGTGAGTGAATCATTGAGAGCAAAACACAGAGAGAGGCC 1602  
 QY 230 oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGlu 250  
 DB 1603 TACTGGGATGTTAGATGTCGTATCATGAAGCCGACATTCGACTAC---AGTAGACAACA 1659  
 QY 250 uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa 264  
 DB 1660 GATTTCTCTTTCTGGAGAATCTGAGTGTCTCAGAGCAAGAGAAAATTCCTCCACTA 1719  
 QY 264 lSerTyxLysValTrpPheTrpValGlyGlyValGluLeuSerProGlu-----GlyIle 282  
 DB 1720 TCAGGTGACCTTGCAGGAGCTGACAGAGGAGGAAAGCCATGACACAGAACATCACAGGACA 1779  
 QY 282 eThrCysCysSerLeuIleProSerGlyAlaGluTrpAla---ArgValSerAlaVa 301  
 DB 1780 CACTCTCTGGACACAGCATTCATTCAGAACCCGAAATTTGGGCTGTGGCTGTCTGTCAGC 1839  
 QY 301 lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe 319  
 DB 1840 AAATTCAAAGAGCGATTTCTGCCCCACTGTTATTAATATGACCTGTGTGGGAGG 1899  
 QY 319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuVa 339  
 DB 1900 GTTGTGTGCTCTCTGCCAGGTCTCTGCAAACTCA---GAGGGCATGGACAACATTCCTGT 1956  
 QY 339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl 356  
 DB 1957 GACTTGGAGCGCTCCAGAGAAAGATCCCTCTGCTGTTTCAGAGTACGTGGTGAATGAG 2016  
 QY 356 aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProG 373  
 DB 2017 AGAGTCTCATCCAGGGGTGACACACAGGTCCCTCTAACTGGCTACGAGTCCGACCCTA 2076  
 QY 373 yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyxArgIleThrVa 393  
 DB 2077 CAATGTGTCTGCTCTGATTTTCAGAGAACATAAAATCTTACATCTGTTATGAATCCGTGT 2136  
 QY 393 lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluG 413  
 DB 2137 GTATCACTCTCAGGGAT---CAAGAGGAGTGCAGCTCCATCTCTGGTAACTTAAAGA 2193  
 QY 413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr 433  
 DB 2194 CAAAGCACCATGAGTGGCCCCCACCACATTAATGCCATCACAGAG---GAAAGGGGAGCAT 2250  
 QY 433 oAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyxTh 453  
 DB 2251 TTTAATTTTCATGAACAGCATTCAGTCCAGGAGCAAAATGGGCTCCCTCCTCATATAG 2310  
 QY 453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467  
 DB 2311 GATATCTGGAAGGAGGAGGAGCTCCAACTCCAGGCTCAGCTCTGTGAATTCCTACAG 2370  
 QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487  
 DB 2371 AGTCTCCCAAAATTCACATCAATAAAGCAGCTCGAG---CCCCGAGTGACATATGTCCT 2427



```

Qy 487 uTrpValThrAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHi 507
Db 2428 GTGGATGACAGCTCTGACAGCTGCTGGTGAAGATTTCCACCGAAATGACAGGAATTTTG 2487
Qy 507 sLeuProAspAsnThr-LeuArgTrpLysValLeuPro-----GlyIleLeuPheL 524
Db 2488 TCTGCAGGTAAAGCAATTTGATGCGGTTTGTGGCACCAGCAATTTGCATTGCTATCAT 2547
Qy 524 euTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyH 544
Db 2548 CATGGTGGGCATTT-----TCTCAACGCATTACTTCCAGCAAAAGTGTGTTGT 2595
Qy 544 isLeuArgHisLysValLeuProArgTrpValTrpGlnLysValProAspProAlaAsnS 564
Db 2596 T-CTCCTAGCAGCCCTCAGACCTCAGACCTCAGTGTGTAGCAGAGAAATTCAGATCCAGCAAATA 2654
Qy 564 erSerSerGlyGlnProHis-----MetGlnValProGluAlaGlnP 579
Db 2655 GCATTTGGCTTAGAAATATCCCATTCGAGAGGAGAAAGACACAGCTGCCCTTGGACAGGC 2714
Qy 579 roLeuGlyAspLeuProIleLeuGluValGluGluMetGluProPro----- 595
Db 2715 TCCTGATAGACTGGCCCAACGCTGAA-----GATCCTGAACCGCTGGTCA 2762
Qy 596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu----- 609
Db 2763 GTGAAGTCTTTCA-TCAAGTGACCCAGTTCAGACATCCGCCCTGCTCCAACTGGCCA 2821
Qy 610 -----AspSerGlyTyr-GluLysHisPheLeuProThrPro 621
Db 2822 CAAGGGGAAAAGGATCCAGGTCAATCAGGCTCTGAGAAAGACATGATGACAGTGCC 2881
Qy 622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
Db 2882 TCA-----AGCCCAACCACTCCAGAGCTCTC 2908

RESULT 13
US-09-949-016-1887
; Sequence 1887, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1887
; LENGTH: 4040
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1887

Alignment Scores:
Pred. No.: 2,02e-20 Length: 4040
Score: 381.50 Matches: 189
Percent Similarity: 38.18% Conservative: 92
Best Local Similarity: 25.68% Mismatches: 285
Query Match: 10.91% Indels: 172
DB: 4 Gaps: 35

US-10-088-950A-1 (1-636) x US-09-949-016-1887 (1-4040)

Qy 12 TrpProLeuProLysLeuAla-Leu-----LeuProLeuTrpValLeuPhe----- 27

```

883	DB	TGCCACTCCCTCAATTCTCAAGTCAAGGTCTTCCCTTGGTACAACTTGTTGTCTG	942
27	QY	-----	27
943	DB	CAAACTGGCCTGTATCAATAGTGAATTCAAATATGTGGACGACAGATCTTCGTTGG	1002
28	QY	----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyrGlyValGlyPr	46
1003	DB	TGTTGCTCCAGAACAGCCTCAAAAT-----TTATCTGTCATACAGAAGCGAGA	1050
46	QY	oLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp-----	59
1051	DB	ACAGGGAGTGTGGCCCTGCACCTCTGGAAAGAGGACGACGCCCATTTATACACTGAGTA	1110
60	QY	-----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln-----	71
1111	DB	TACTCTACAGCTAAGTCGACCAAAAATTTAACTGCGCAGAAGCAATGTAAGACATTTA	1170
72	QY	-----LysTyrArgSerAsnIysTh	78
1171	DB	TTGTGACTATTTGGACTTTGGAATCAACCTCACCCCTGAATCACTCGAATCCAAATTCAC	1230
78	QY	xGlnThrVal---AlaValalalaGlyArgSerTrpValalalleProArgGluGlnLe	97
1231	DB	AGCCAAGTTACTGCTGCTCAATGCTGTGAAGACTCTCTTCTACTTCCA---TCCACATT	1287
97	QY	uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr	117
1288	DB	CACATTTCTGGACATAGTG-----AGGCCTCTT---CTCC	1320
117	QY	oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa	137
1321	DB	GTGGACATTAGTAATCAAAATTTCAA---AAGGCTTCTGTGAGCAGA-----	1363
137	QY	lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr	157
1364	DB	-----TGTAACCTTTATTGGAGA-----GA	1383
157	QY	oSerHisLysValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpTh	177
1384	DB	TGAGGAGCTGGTACTGCTTAATCGACTAGATATCGGCCAGTAACAGCAGGCTCTGGAA	1443
177	QY	rLeuLeuGluProGluLeuIysThrLeProLeuTrpProVal-----GluIl	193
1444	DB	TATG-----GTTAATGTTACAAAGGCCCAAGAGACATGATTT	1482
193	QY	eGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGl	213
1483	DB	GCTGGATCTTCAAAACCAATTTACAAATATGAATTTACATTTCTCTAAGCTACATCTTA	1542
213	QY	uGluAspLeuTrpGluTrpSerProIleLeuSerPheGlnThrPro-----Pr	230
1543	DB	TAGGGAGTTGGAGTATGGAGTGAATCATTTGAGAGCAAAACACCAAGAAGAGGCC	1602
230	QY	oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGl	250
1603	DB	TACTGGAGCTGTAGATGCTCTGGTACATGAACCGGCACATTTGACTAC---AGTAGACAACA	1659
250	QY	uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa	264
1660	DB	GATTTCTCTTTCTTGGAGAATCTGAGTGCTCTCAGAGGCAAGGAAAAATTTCTCCACTA	1719
264	QY	lSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu-----GlyIl	282
1720	DB	TCAGGTGACCTTCGAGGAGCTGACAGAGGGAAGCCATGACACAGAACATCACAGACA	1779
282	QY	eThrCysCysSerLeuIleProSerGlyAlaGluTrpAla---ArgValSerAlaVa	301
1780	DB	CACCTCTCGGCACACAGTCATTCCTAGAACCGGAAATTTGGCGTGTGCGTGTGTCGACG	1839
301	QY	lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe	319
1840	DB	AAATTTCAAAAGGCGATTTCTCGCCCACTCGTATTATTAACATAATGAACCTGTGAGCAGG	1899

US-10-088-950A-1 (1-636) x US-09-949-016-1887 (1-4040)

Qy 12 TrpProLeuProLysLeuAla-Leu-----LeuProLeuLeuTrpValLeuPhe----- 27

QY  
301 TAAATA-----TATCTGTTGGTGTGAGGCAGG 1899

Dbb  
1840 AAATTCAAAGGCGAGTTCCTGCCCACTCGTATTAAACATTAATGAACCTGTGAGGCAGG 1899

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319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa 339
1900 GTTGTGGCTCTCGCAGGTCTCTGCAAACTCA---GAGGGCATGAGCAACACTCTGGT 1956
339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValAlaSerTrpAl 356
1957 GACTTGGCAGCTCCAGGAAAGATCCCTCTCTGTCTACGGAGTACGTGGTGGAAATGAG 2016
356 aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProProG1 373
2017 AGAGTCCATCCAGGGGGTGACACACAGGTCCTCTTAACCTGCTACGGAGTCGACCTTA 2076
373 yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyArgIleThrVa 393
2077 CAATGTCTGCTCTGATTTCAGAGAACATAAAATCCTACATCTGTATGAATCCGTGT 2136
393 lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluG1 413
2137 GTATGCACTCTCAGGGAT---CAAGGAGGATGAGCTCCATCTCTGGTGAATCTTAAGCA 2193
413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr 433
2194 CAAGACACCACTGAGTGGCCCCACATTAATGCCATCACAGAG---GAAAAGGGGAGCAT 2250
433 oAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyTh 453
2251 TTTAATTTCAATGAACAGCATTCAGTCCAGGAGCAAAATGGGCTGCTCTCCATATAG 2310
453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467
2311 GATATACGGAAGAACGAGGACTCCAACTCCAGCTCAGCTCTGTAATTCCTTACAG 2370
467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
2371 AGTCTCCCAAAATTCACATCCATAAAGACGCTGCAG---CCCGAGTGACATATGCTCT 2427
487 uTrpValThrAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHi 507
2428 GTGGATGACAGCTCTGACGCTGCTGGTGAAGTTCACCGAAATGACAGAGGAATTTTG 2487
507 sLeuProAspAsnThr-LeuArgTrpLysValLeuPro-----GlyIleLeuPheLe 524
2488 TCTCAAGGTAAACCAATGGATGGGTGTGTGGCACCAGCATTTGCATTCATCAT 2547
524 euTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyTh 544
2548 CATGTTGGGCATT---TCTCAACACATTAATCTCCAGCAAAAGGTGTTGT 2595
544 isLeuArgHisLysValLeuProArgTrpValTrpGlyLysValProAspProAlaAsnS 564
2596 T-CTCCTAGCAGCCCTCAGACCTCAGTGGTGTAGCAGAGAAATTCAGATCCAGCAATA 2654
564 erSerSerGlyLysProHis-----MetGluGlnValProGluAlaGlnP 579
2655 GCATTGGCTGAGAAATATCCCATTCAGAGGAGAGACACAGCTCCCTTGGACAGGC 2714
579 roLeuGlyAspLeuProIleLeuGluValGluGluMetGluProProPro----- 595
2715 TCCTGATAGACTGGCCCAAGCCTGAA-----GATCCTGAACCCGCTGTATCA 2762
596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu----- 609
2763 GTGAAGTCTTCA-TCAAGTACCCAGTGTTCAGACATATCCCTCTGCTCCAACCTGCCA 2821
610 -----AspSerGlyTyTr-GluLysHisPheLeuProThrPro 621
2822 CAAGGGGAAAGGAATCAAGGTTCATCAGGCTCTGTGAAAGACATGATGCACAGTGCC 2881
622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
2882 TCA-----AGCCACCACTCCAGAGCTCTC 2908
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RESULT 14
US-07-923-976-3
; Sequence 3, Application US/07923976
; Patent No. 5574136
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigekazu
; APPLICANT: Fukunaga, Rikio
; TITLE OF INVENTION: DNA Encoding Granulocyte
; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones, Tullar & Cooper, P.C.
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/923,976
; FILING DATE: 19920922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74539/1990
; FILING DATE: 23-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 176629/1990
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP91/00375
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hellwege, James W.
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 514853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2943 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 170..2677
; US-07-923-976-3

Alignment Scores:
Pred. No.: 6,88e-14 Length: 2943
Score: 297.50 Matches: 173
Percent Similarity: 34.73% Conservative: 76
Best Local Similarity: 24.13% Mismatches: 269
Query Match: 8.50% Indels: 201
DB: 1 Gaps: 33

US-10-088-950A-1 (1-636) x US-07-923-976-3 (1-2943)
QY 50 LeuAsnCysSerTrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGln 69
Db 587 CTCATCTGCCAGTGGGAGCCAGGACCTGAGACCCACCTACCCAGCTTCACTCTGAAG 646
QY 70 SerGlnLysTyArgSerAsn---LysThrGlnThrValAlaVal----- 83
Db 647 AGTTTCAAGAGCGGGGCAACTGTGAGACCCAGGGGACTCCATCTGTGACGTGGTCCC 706
QY 84 AlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSerAspLysLeu 103
Db 84 AlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSerAspLysLeu 103
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Db 707 AAGGCGGCGAGAGCCACCTGTCATCCACGCAACACCTGCTGTGTACCAAGATATG 766  
Qy 104 LeuValTrp-----GlyThrLysAlaGlyGlnProLeuTrp--- 115  
Db 767 GGCATCTGGGTGAGGAGAGATGCGCTGGGGACAGCATGTCCCAACACTGTGTCT 826  
Qy 116 -----ProProValPheValAsnLeuLeuGlnMet 126  
Db 827 GATCCCATGGATGTTGTGAACACTGGAGCCGCCCATGCTGCGGACCATGGAGCCGCCT 886  
Qy 127 LysProAsnAlaProAsgLeuGly-----ProAspValAspPhe 139  
Db 887 GAAGGGCCCTCCCAAGAGAGGCTGCTCAGCTGTGCTGGAGCCA----- 934  
Qy 140 SerGluAspProLeuGluAlaThrValHisTrpAlaProProTrpProSerHis 159  
Db 935 -----TGGCAGCCAGGCGCTGCACATAAATCAG 961  
Qy 160 LysValLeuIleCysGlnPhe-----HisTyrArgArgCysGlnGluAlaAlaTrpThrLeu 178  
Db 962 AAG-----TGTGAGCTCGGCACAAAGCGCGAGCTGGAGAGCCAGCTGGGCACCTG 1012  
Qy 179 LeuGluProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeu 198  
Db 1013 GTGGGCCCC-----CTCCCTTGGAGGCGCTTCAGTATGAGCTC 1051  
Qy 199 -----AlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213  
Db 1052 TGGGGCTCTCCAGCCAGCGCTACACCTGCAGATACGCTGCATCCGCTGGCCCTG 1111  
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThr-ProProSerAlaPr 233  
Db 1112 CCTGGCACTGGAGCGACTGGAGCCCGAGCTGGAGCTGAGAACTACCGAAGCGGCCCC 1171  
Qy 233 oLysAspValTrpValSerGlyAsnLeuCysGly-----ThrProGlyGlyGluGluPr 251  
Db 1172 ACTCTCAGCTGGACACATGTTGGCGGAGGAGGCTGGAGCCCGCA-----CAGTG 1225  
Qy 251 oLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTr 271  
Db 1226 -CAGCTGTTCTGGAG---CCAGTGGCCCTGGAGGAGACAGCGGAGTCCAGGTTA 1281  
Qy 271 pValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIleProse 291  
Db 1282 TGTG-----GTTTCTTGGAGACCTC 1302  
Qy 291 rGlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAs 311  
Db 1303 AGGCGAGGCTGGGCGCCATCTGCCCTCTGCAACACACAGAGCTCAGCTGCACCTTCCA 1362  
Qy 311 nLeu-----SerLeuValCysLeuAspSerAla-----SerAl 322  
Db 1363 CCTGCTTCAGAACCCAGGAGGTGGCGCTTGTGGCTATTAACCTCAGCGGACCTCTCG 1422  
Qy 322 aProArgSerValAlaValSerIleAlaGlySerThr----- 335  
Db 1423 CCCCACCGGTGTCTTCTCAGAAAGCAGAGGCGCCAGCTCTGACCAGACTCCATGCCAT 1482  
Qy 336 -----GluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuG 350  
Db 1483 GGCCCGAGACCTCAGACGCTCTGGTAGGTGGAGTGGAGCCCGCAATCCATGGCGCTCAGG 1542  
Qy 350 uHisValValAspTrpAlaArgAspGlyAspProLeuGluLysLeuAsn-----TrpVa 368  
Db 1543 CTATGTGATTGAGTGGGCGCTGGGCGCCCGCCAGCGCGAGCMATAGCAAGACCTGGAG 1602  
Qy 368 lArgLeuProProGlyAsnLeuSerAla---LeuLeuProGlyAsnPheThrValGlyVa 387  
Db 1603 GATGAACAGAAATGGAGAGCCACGGGTCTTCTCTGAAGGAGAAATCAGGCGCTTCA 1662  
Qy 387 lProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerVa 407  
Db 1663 GCTCTATGAGATCATCTGATCCCTTGTATACCAGGACACCATCGGACCCCTCCAGCATG 1722

Qy 407 lTrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAs 427  
Db 1723 CTATGCTACTCTCAAGAAATGCTCCTCCATGCCCCAGAGCTG---CATCTAAAGCA 1779  
Qy 427 pAlaProProGlyThrProAlaIleAlaTrpGlyValProArgHisGlnLeuArgL 447  
Db 1780 CATTTGGCAAGACCTGGGCACAGCTGGAGTGGTGGCTGAGCCCTGAGCTGGGGAAG 1839  
Qy 447 yHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThrSerProSerValCysMetAs 467  
Db 1840 CCCCCTTACCACCTACACCATCTTCTGGACCAAGCTCAGAACCCAGCTCTCTCCGCCAT 1899  
Qy 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487  
Db 1900 CTTGAATGCTCTCTCCGCTGGCTTGTCTCCATGGCTGAG-----CCCCCAGCTCT 1953  
Qy 487 uTrp-----ValTh 490  
Db 1954 GTATCATCATCCACTCATGCTGCAGCAGAGCTGGGGCCCAACCAAGTACAGTCTCCAC 2013  
Qy 490 rAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAs 510  
Db 2014 CTGATGACCTTGACCCAGAGGGGTG-----GAGCTACACATC----- 2053  
Qy 510 pAsnThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeu 530  
Db 2054 -----ATCTGGGCTGTTCGGCTCTCTGCTGTT 2082  
Qy 530 u-----GlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArgHi 547  
Db 2083 GCTCACCTGCTCTGTGGA-----ACTGCTGCTCTGTGTGCGACCCCAACAG 2130  
Qy 547 sLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerGl 567  
Db 2131 GAAG-----ATCCCTCTGGCCCAAGTGTCCAGACCCAGCTCAGCAGCAGCTGGG 2181  
Qy 567 Y-----GlnProHisMetGluGlnValPro-----GluAlaGl 578  
Db 2182 CTCTGGGTGCCCCACAATCATGAGGAGGATGCTTCCAGCTGCCGCGCTTGCACGCC 2241  
Qy 578 nProLeuGlyAspLeuProIleLeuGluValGluGluMetGluProPro----- 595  
Db 2242 ACCATCACCAGCTCAGAGTGTGGAGGAGTGAAGAAGCGCGTGCCTGGAGTC 2301  
Qy 596 -----ValMetGluSe 599  
Db 2302 CCATAACAGCTCAGAGACCTGTGGCTCCCACTCTGTGGTCCAGACCTATGTCTCCAGG 2361  
Qy 599 rSerGlnProAlaGlnAlaThrAlaPro---LeuAspSerGlyTyrGlyLysHisPheLe 618  
Db 2362 GGACCCNAGAGCAGTTTCCACCAGCCCAATCCAGTCTGGCACCAGCATCAGGTCT 2421  
Qy 618 u-----ProThrProGluGluLeuGlyLeuGlyPro----- 629  
Db 2422 TTATGGCAGCTGTGGGAGGAGCCCAAGCCAGGCGCCAGGCA-CTATCTCGCTGTG 2480  
Qy 630 -----ProArgProGlnValLeu 635  
Db 2481 ACTCCACTCAGCCCTCTTGGCGGGCTCTACCCCGGAGCCCAAGTCTCTA 2529

## RESULT 15

US-09-023-655-1086

; Sequence 1086, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

Fri Feb 25 10:29:30 2005

ADDRESS: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1086:

SEQUENCE CHARACTERISTICS:

LENGTH: 2943 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g183046

US-09-023-655-1086

Alignment Scores:

Pred. No.: 6.88e-14 Length: 2943  
Score: 297.50 Matches: 173  
Percent Similarity: 34.73% Conservative: 76  
Best Local Similarity: 24.13% Mismatches: 269  
Query Match: 8.50% Indels: 201  
DB: 4 Gaps: 33

US-10-088-950A-1 (1-636) x US-09-023-655-1086 (1-2943)

QY 50 LeuAsnCysSerTrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGln 69  
DB 587 CTCATCTGCCAGTGGGAGCCAGGACCTGAGACCCACCTACCCAGCTTCACTCTGAAG 646  
QY 70 SeGlnLysTrpArgSerAsn---LysThrGlnThrValAlaVal-----83  
DB 647 AGTTTCAAGACCGGGGCAACTGTGACACCCCAAGGGGACTCCATCTGGAGCTGGTGGCC 706  
QY 84 AlaAlaGlyArgSerTrpValAlaIleProArgGlnLeuThrMetSerAspLysLeu 103  
DB 707 AAGACGGGAGAGCCACTGCTGATCCACGCAACACCTGCTGTTGTACCAAGATATG 766  
QY 104 LeuValTrp-----GlyThrLysAlaGlyGlnProLeuTrp---115  
DB 767 GGATCTGGGTGGGAGAGAGATGCGTGGGAGCAGCATGTCCCAACAACCTGTGTCTT 826  
QY 116 -----ProProValPheValAlaLeuLeuGluThrGlnMet 126  
DB 827 GATCCCATGGATGTTGAAACTGGAGCCCCCATGTGGGACCATGGAGCCCT 886  
QY 127 LysProAsnAlaProArgLeuGly-----ProAspValAspPhe 139  
DB 887 GAAGGGGCCCCCTCCCGAGGAGGCTGCTACAGCTGTGTGGAGCCA-----934  
QY 140 SerGluAspAspProLeuGluAlaThrValHisTrpAlaProProTrpProSerHis 159  
DB 140 SerGluAspAspProLeuGluAlaThrValHisTrpAlaProProTrpProSerHis 159

Db 935 -----TGGCAGCCAGGCGCTGCACATAAATCAG 961  
QY 160 LysValLeuIleCysGlnPhe---HisTyrArgArgCysGlnGluAlaIleTTPThrLeu 178  
Db 962 AAG-----TGTGAGCTGGCCCAAGCCGCGTGGAGAACCCACTGGGCACTG 1012  
QY 179 LeuGluProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeu 198  
Db 1013 GTGGGCCCC-----CTCCCTTGGAGGCGCTTCAATAGTATGAGCTC 1051  
QY 199 -----AlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213  
Db 1052 TGGCGGCTCTCCAGCCAGCGCTACACCTCAGATACGCTGCATCCGCTGGCCCTG 1111  
QY 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThr-ProProSerAlaPr 233  
Db 1112 CTGGCCACTGGAGCGACTGGAGCCCCCAGCTGGAGCTGAGAACTACCGAAGGGCCCC 1171  
QY 233 oLysAspValTrpValSerGlyAsnLeuCysGly-----ThrProGlyGlyGluGluPr 251  
Db 1172 ACTGTCAGACTGGACACATGTTGGCGGAGGCGAGGCTGGACCCAGCA-----CAGTG 1225  
QY 251 oLeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTTPPheTr 271  
Db 1226 -CAGCTGTTCTGAAG---CCAGTGGCCCTGGAGGAAGACAGCGAGGATCCAAAGTTA 1281  
QY 271 pValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysCysSerLeuIleProSe 291  
Db 1282 TGTG-----GTTTCTGGAGACCTC 1302  
QY 291 rGlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAs 311  
Db 1303 AGCCAGGCTGGGCGCATCTGCCCCCTCTGCACACACACAGAGCTGAGTGCACCTTCCA 1362  
QY 311 nLeu-----SerLeuValCysLeuAspSerAla-----SerAl 322  
Db 1363 CTGCTTTCAGAACCCAGAGGTTGGCCCTTGTGGCTATTAACCTACGCGGAGCTCTCG 1422  
QY 322 aProArgSerValAlaValSerIleAlaGlySerThr-----335  
Db 1423 CCCACCCCGTGGTCTTCTCAGAAAGCAGAGGCGCCAGCTCTGACAGACTCCATGCCAT 1482  
QY 336 -----GluLeuLeuValThrTTPGlnProGlyProGlyGluProLeuGlu 350  
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QY 387 lProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerVa 407  
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QY 407 lTrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAs 427  
Db 1723 CTATGCTACTCTCAAGAAATGGCTCCCTCCATGCCCGAGAGCTG---CATCTAAGCA 1779  
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QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487  
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Qy 596 -----ValMetGluSe 599
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2362 GGACCCAAAGACGAGTTTCCACCCAGCCCAATCCAGTCTGGCACCGGATCAGGTCCT 2421
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Qy 630 -----ProArgProGlnValLeu 635
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Search completed: February 23, 2005, 08:59:50  
Job time : 360 secs





GenCore version 5.1.6  
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Run on: February 23, 2005, 05:04:23 ; Search time 928 Seconds  
(without alignments)  
4050.728 Million cell updates/sec

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Perfect score: 3498  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO.spool/US10088950/runat\_18022005\_094501\_21875/app\_query.fasta\_1.775  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	3498	100.0	2646	18	US-10-663-158-3	Sequence 3, Appli
2	3498	100.0	2657	17	US-10-351-157-8	Sequence 8, Appli
3	3498	100.0	2657	17	US-10-352-554-8	Sequence 8, Appli
4	3498	100.0	2663	17	US-10-172-118-1092	Sequence 1092, Ap
5	3498	100.0	2663	17	US-10-342-887-1092	Sequence 1092, Ap
6	3498	100.0	3258	18	US-10-755-889-163	Sequence 163, App
7	3494	99.9	2628	10	US-09-791-497-13	Sequence 13, Appl
8	3494	99.9	2628	13	US-10-000-776-11	Sequence 11, Appl
9	3494	99.9	2628	18	US-10-777-790-11	Sequence 11, Appl
10	2044	58.4	2005	18	US-10-663-158-4	Sequence 4, Appli
11	381.5	10.9	4040	18	US-10-370-715B-67	Sequence 67, Appl
12	331	9.5	4023	17	US-10-398-666-11	Sequence 11, Appl
13	297.5	8.5	2943	17	US-10-641-643-1086	Sequence 1086, Ap
14	297.5	8.5	3139	16	US-10-252-157-457	Sequence 457, App
15	288.5	8.2	4026	17	US-10-351-157-134	Sequence 134, App
16	288.5	8.2	4026	17	US-10-352-554-119	Sequence 119, App
17	250	7.1	3085	15	US-10-177-293-229	Sequence 229, App
18	250	7.1	3085	17	US-10-172-118-736	Sequence 736, App
19	250	7.1	3085	17	US-10-295-027-73	Sequence 73, Appl
20	250	7.1	3085	17	US-10-058-270A-31	Sequence 31, Appl
21	250	7.1	3085	17	US-10-342-887-736	Sequence 736, App
22	250	7.1	3085	17	US-10-641-643-1131	Sequence 1131, Ap
23	250	7.1	3358	14	US-10-116-802-208	Sequence 208, App
24	250	7.1	7754	16	US-10-240-965-26	Sequence 26, Appl
25	250	7.1	7819	10	US-09-971-392-19	Sequence 19, Appl
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27	250	7.1	7819	16	US-10-252-157-252	Sequence 252, App
28	249.5	7.1	2995	16	US-10-425-529-17	Sequence 17, Appl
29	249.5	7.1	2995	19	US-10-645-012-17	Sequence 17, Appl
30	248	7.1	2369	15	US-10-313-135-1	Sequence 1, Appli
31	237.5	6.8	2964	17	US-10-352-554-6	Sequence 6, Appli
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34	215.5	6.2	3477	9	US-09-313-942-25	Sequence 25, Appl
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44	207	5.9	2119	15	US-10-006-265-16	Sequence 16, Appl
45	207	5.9	2402	10	US-09-892-949-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-10-663-158-3  
; Sequence 3, Application US/10663158  
; Publication No. US20040234522A1  
; GENERAL INFORMATION:  
; APPLICANT: Desauvage, Frederic  
; APPLICANT: Grewal, Iqbal  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCOR  
; FILE REFERENCE: 11669.123USC1  
; CURRENT APPLICATION NUMBER: US/10/663,158  
; PRIOR FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 09/692,504  
; PRIOR FILING DATE: 2000-10-18  
; CURRENT APPLICATION NUMBER: US 60/160,542  
; PRIOR FILING DATE: 1999-10-20  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2646

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2433)..(2433)
; OTHER INFORMATION: n is a, c, t, or g
US-10-663-158-3

Alignment Scores:
Pred. No.:      8,34e-310      Length:      2646
Score:          3498.00      Matches:      636
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              18          Gaps:      0

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QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
DB 172 CCTCTGTTCTGGGTGCTTTTCCAGCGGACGCGTCCCGAGGCGCGCGGCGCACTGCGAG 231
QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAnCysSerTrpGluProLeuGlyAspLeu 60
DB 232 TGCTACGGAGTTGGACCCCTTGGGCGACTTGAACCTGCTCGTGGAGCGCTTCTGGGACCTG 291
QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
DB 292 GAGGCCCTCTCGAGTTACCTCTCCAGAGCCCAAGTACCTGTTCCAAACCAACCCAGACT 351
QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
DB 352 GTGGCAGTGGCAGCGGAGCGAGCTGGGTGGGCATTCCTCTCGGGAACAGCTCACCATGCT 411
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QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
DB 472 AACCTAGAACCCCAATAGAACCAACGCCCGCGCTGGGCGCTGACGTGACATTTTCC 531
QY 141 GluAspAspProLeuGluAlaThrValHisTyrAlaProProThrTrpProSerHisLys 160
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QY 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
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QY 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
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## RESULT 2

US-10-351-157-8  
; Sequence 8, Application US/10351157  
; Publication NO. US20030215838A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Kuijper, Joseph L.  
; APPLICANT: Dasovich, Maria M.  
; APPLICANT: Grant, Francis J.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Hammond, Angela K.  
; APPLICANT: No. US20030215838A1ak, Julia E.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Dillon, Stacey R.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
; FILE REFERENCE: 02-02  
; CURRENT APPLICATION NUMBER: US/10/351,157  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/435,361  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/389,108  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/350,325  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2657  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (133)...(2040)  
US-10-351-157-8

## Alignment Scores:

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Score: 3498.00 Matches: 636  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 17 Gaps: 0

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QY	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
DB	313	GGAGCCCCCTCCGAGTTTACACCTCCAGAGCAAAAGTACCGTTCCCAACAAACCCAGACT	372
QY	81	ValAlaValAlaAlaGlyArgSerTrpValAlaAlaProArgGluGlnLeuThrMetSer	100
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QY	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal	120
DB	433	GACAACTCTTGTCTGGGGCACTAAGCAGCGGCGGCTCTCTGGCCCCCGCTTTCGTG	492
QY	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspPheSer	140

DB	493	AACCTAGAAACCCAAATGAAGCCAAAGCGCCCCGGCTGGCGCTGACGTGGAGCTTTTTC	552
QY	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
DB	553	GAGGATGACCCCTCGGAGGCCACTGTCCATTTGGGCCCCACTACATGGCCATCTCATAA	612
QY	161	ValLeuLeuCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
DB	613	GTTCTGATCTGCCAGTTTCCACTACCGAAGATGTCCAGGAGCGGCTGGAGCCCTGCTGAA	672
QY	181	ProGluLeuLysThrLeuProLeuThrProValGluLeuGlnAspLeuGluLeuAlaThr	200
DB	673	CCGAGCTGAAGACCATACCCCTGAGCCCTGTGTGAGATCCAGATTTGGAGCTAGCCACT	732
QY	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp	220
DB	733	GGGTACANAGTGTATGGCCGCTCCCGATGGAGAGAGAGAGATTTGTGGGGCGAGTGG	792
QY	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
DB	793	AGCCCATTTTGTCTTCCAGACACCGCTTCTGCTCCAAAGATGTGTGGGTATCAGGG	852
QY	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro	260
DB	853	AACCTCTGGGAGCGCTGGAGGAGAGAACCTTTGCTTATGGAAGGCCCCAGGGGCC	912
QY	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
DB	913	TGTGTGAGGTGAGCTACAAAGTCTGGTCTGGGTTGGAGTCTGTGAGCTGAGTCCAGAA	972
QY	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
DB	973	GGAAATTACCTGTCTGCTCCCTAAATTCAGTGGGCGGAGTGGGCGAGGCTGTCGCT	1032
QY	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
DB	1033	GTCAACGCCACAGCTGGGAGCGCTCTCACCAACCTCTCTTGTGCTGCTTGGATTCAGCC	1092
QY	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
DB	1093	TCTGCCCCCGTAGCTGGAGTACAGAGATCGCTGGGAGCAGGAGCTACTTGGTGACC	1152
QY	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
DB	1153	TGGCAACCGGGGCTGGGAAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC	1212
QY	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
DB	1213	CCCTGGAGAAACTCAACTGGGTCCGGCTTCCCGCTGGGAACCTCAGTGTCTGTACCA	1272
QY	381	GlyAsnPheThrValGlyValProTyrArgIleThrValAlaValSerAlaSerGly	400
DB	1273	GGAAATTCACGTCTGGGGTCCCTATCGAATCACTGTGACCGAGTCTCTGTCTCAGGC	1332
QY	401	LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
DB	1333	TTGGCTCTGTCATCTCTCGCTGGGGGTTCCAGGAGGAATTAGCACCCCTAGTGGGGCCA	1392
QY	421	ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal	440
DB	1393	ACGCTTTGGCGACTCCAGATGCCCCCTCCAGGGAGCCCGGCCCATAGCTGGGGAGAGTC	1452
QY	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
DB	1453	CAAAGGCACAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGACAGAGTGGAAACC	1512
QY	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
DB	1513	AGCCCCCTCGTCTGCATGAATGTGAGTGGCAACACACAGAGTGTCCACCTCGCTGACCTT	1572
QY	481	ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
DB	1573	CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCTGCTGGAGAGGGCCCTCT	1632

```
QY 501 GlyProIleLeuAArgLeuHisLeuProAspLeuThrLeuAArgTrpLysValLeuProGly 520
DB 1633 GGTCCCATCTCCGGCTTCATCTACAGATAACACCTTGAGTGGAAAGTTCTGCCAGGC 1692
QY 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
DB 1693 ATCCATTCTTGTGGGGCTGTGTCTGTGGGGTGTGGCCCTGAGCTGGCCACCTCTCGA 1752
QY 541 ArgCysTyrHisLeuAArgHisLysValLeuProAArgTrpValTrpGluLysValProAsp 560
DB 1753 AGTGCTACCACTTAAGGCACAAAGTGTGCCCGCTGGGTCCTGGAGAAAAGTTCTCGAT 1812
QY 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
DB 1813 CTTGCCAACAGCAGTTCAGGCCAGCCACACATGGAGCAAGTACCTGAGGGCCAGCCCTT 1872
QY 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600
DB 1873 GGGGACTTGTCCCATCTCGAAGTGGAGGATGGAGCCCCCGCCGGTTATGGAGTCTCTCC 1932
QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
DB 1933 CAGCCCGCCAGCCACCCCGCTTGACTCTGGGTATGAGAGCACTTCTCTGCCACA 1992
QY 621 ProGluGluLeuGlyLeuLeuGlyProProAArgProGlnValLeuAla 636
DB 1993 CCTGAGGAGCTGGGCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTGGCC 2040
```

## RESULT 3

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US-10-352-554-8
; Sequence 8, Application US/10352554
; Publication No. US20030224487A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Novak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
; FILE REFERENCE: 02-01
; CURRENT APPLICATION NUMBER: US/10/352,554
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/375,323
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/435,315
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)...(2040)
US-10-352-554-8
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Alignment Scores:
Pred. No.: 8,386-310 Length: 2657
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
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US-10-088-950A-1 (1-636) x US-10-352-554-8 (1-2657)

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QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
DB 133 ATGCGGGAGGAGGCGGCGCCCTTCTGGCTGTGGCGCTGCCCAAGCTGGCGCTGCTG 192
QY 21 ProLeuLeuTrpValLeuPheGlnAArgProGlnGlySerAlaGlyProLeuGln 40
DB 193 CCTCTGTGTGGGTGCTTTTCCAGCGGACGCTCCCGAGGCGAGCGCGGCGACCTGCAG 252
QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
DB 253 TGCTACGGAGTGGACCTTGGGCGACTGAACCTGCTCGTGGGAGCCTCTTTGGGAGACTG 312
QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
DB 313 GGAGCCCTCTCCGAGTTACCTCCAGAGCCAAAGTACCGTTCACAAACAAACCCAGACT 372
QY 81 ValAlaValAlaAlaGlyAArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
DB 373 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGGAACAGCTCACCATGTCT 432
QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120
DB 433 GACAAACTCTCTGTCTGGGCACTAAAGCAGCGCAGCTCTCTGGCCCCCGCTTCTGTG 492
QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
DB 493 AACCTAGAACCCAAATGAGCCAAACGCCCGCTGGGCCCTGACGTGGACTTTTCC 552
QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
DB 553 GAGGATGACCCCTGGAGGCACCTGTCCATTGGGCCCCACCTACATGGCCATCTCAATAA 612
QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180
DB 613 GTTCTGATCTGCCAGTCTCCACTACCAAGATGTCCAGAGGCGGCTGGACCTCTCTGGA 672
QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
DB 673 CCGGAGCTGGAAGACATACCCCTGACCCCTGTTCAGATCCCAAGATTGGAGCTAGCCACT 732
QY 201 GlyTyrLysValTyrGlyArgCysArgMetCulLysGluGluAspLeuTrpGlyGluTrp 220
DB 733 GGCTACAAAGTGTATGGCCGCTGCGGATGAGAAAGAGGATTTGTGGGGCGAGTGG 792
QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
DB 793 AGCCCCATTTGTCTCTCCAGACACCCGCTTCTGCTCCAAAAGATGTCTGGGTATCAGG 852
QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPro 260
DB 853 AACCTCTGTGGGACGCTGGAGGAGAGAACCTTTGCTTCTATGGAAGGCCCCAGGGGCC 912
QY 261 CysValGlnValSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu 280
DB 913 TGTGTGAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTGTGAGCTGAGTCCAGAA 972
QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300
DB 973 GGAATTACTGTGTGCTCTCCCTAATTCAGTGGGGCGGAGTGGGCCAGGGTGTCCGCT 1032
QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320
DB 1033 GTCAACGCCACAAAGCTGGGAGCCTCTCACCAACCTCTCTTTGGTCTGTGTGATTACGCC 1092
QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340
DB 1093 TCTGCCCGCGTAGGCGTGGCAGTACGACAGATCGCTGGGAGCAGCAGAGCTACTGTGACC 1152
QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360
DB 1153 TGGCAACCGGGGCTGGGGACCACTGGAGCATGTAGTGGATCTGGGCTCGAGATGGGAC 1212
QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380
```

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Db 1213 CCCCTGGAGAACTCAACTGGGTCGGCTTCCCCCTGGGAACCTCAGTGTCTGTACCA 1272
Qy 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400
Db 1273 GGGAAATTCACGTGTGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGCTCAGGC 1332
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420
Db 1333 TTGGCCTCTGCATCTCCGCTCTGGGGTTTCAGGGAGGAATTAGCACCCCTAGTGGGGCA 1392
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440
Db 1393 ACGCTTTGGGCACATCCAAAGATGCCCTCCAGGACCCCGCCATAGCGTGGGAGAGGTC 1452
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460
Db 1453 CCAGGCACACAGCTCTCGAGGCCACCTCACCCACTACACCTTGTGTGCACAGATGGAAACC 1512
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480
Db 1513 AGCCCTTCCTCGATGATGTGAGTGGCAACACACAGAGTGTACCCCTGCCTGACCTT 1572
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500
Db 1573 CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCCT 1632
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520
Db 1633 GGTCCCATCTCTCCGGCTTCATCTACAGATTAACACCTCGAGGTGGAAGTTCTGCCAGGC 1692
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540
Db 1693 ATCTATTCTTGTGGGGCTTGTCTCTGTGGGTGTGGCTGAGCCTGGCCACCTCTGGA 1752
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560
Db 1753 AGGTGCTACCACTTAAGGCACAAAGTGTCTCCCGCTGGGTCTGGGAGAAAGTTCTCGAT 1812
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580
Db 1813 CCTGCCAACAGCATTCAGGCCACCCACATGAGCAAGTACCTGAGGCCACGCCCTT 1872
Qy 581 GlyAspLeuProIleLeuGluValGluMetGluProProProValMetGluSerSer 600
Db 1873 GGGGACTTGCCATCTCTGGAAGTGGAGAGATGGAGCCCGCCGGTTATGGAGTCTCC 1932
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620
Db 1933 CAGCCCGCCAGGCACCGCCCGCTTGACTCTGGGTATGAGAGCACTTCTCTGCCACA 1992
Qy 621 ProGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636
Db 1993 CCTGAGGAGCTGGGCCCTTCTGGGGCCCCCCCCAGGCCACAGGTTCTGGCC 2040
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## RESULT 4

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US-10-172-118-1092
; Sequence 1092, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10172.118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
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; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1092
; LENGTH: 2663
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE accession number: NM_004843
; DATABASE entry date: 2001-06-18
US-10-172-118-1092
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Alignment Scores:
Pred. No.: 8,41e-310 Length: 2663
Score: 3498.00 Matches: 636
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
```

US-10-088-950A-1 (1-636) x US-10-172-118-1092 (1-2663)

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Qy 1 MetArgGlyGlyValArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20
Db 139 ATGGGGGAGGCGAGGGCGGCCCTTCTGGCTGTGGCCGCTGCCAAAGCTGGCGCTGCTG 198
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40
Db 199 CCTCTGTGTGGTGTCTTTTCCAGCGGACCGGTCCCAGGGCAGCGCGGGCCACTGCAG 258
Qy 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60
Db 259 TGTCTACGAGTGTGACCCCTTGGCGCACTTGAACCTGCTCGTGGGAGCCTCTTGGGCACTG 318
Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db 319 GAGAGCCCTCCAGGTTTACACCTCCAGAGCAAAAGTACCCTTCCAAACAAACCCAGACT 378
Qy 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100
Db 379 GTGGCAGTGGCAGCGGAGCGAGCTGGTGGCCATTCTCGGNAACAGCTCACCATTCTCT 438
Qy 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120
Db 439 GACAAACTCTCTCTGGGCACTAAGGAGCGGCAGCCTCTCTGGCCCCCGCTCTCGTG 498
Qy 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db 499 AACCTAGAAACCCAAATGAAGCCAAACGCCCCCGCTGGGCCCTTGACGTGGACTTTTCC 558
Qy 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160
Db 559 GAGGATGACCCCTGGAGGCCACTGTCCATTTGGCCCCCACTACATGGCCCATCTCATAAA 618
Qy 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaIleThrThrLeuGlu 180
Db 619 GTTCTGATCTGCCAGTTCCACTACCGAAGATGTCCAGAGCGCGCTGAGCCCTGCGAA 678
Qy 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200
Db 679 CCGAGAGCTGAAGACCATACCCCTGAGCCCTTGTGAGATCCAAAGATTTGGAGTAGCCACT 738
Qy 201 GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyGluTrp 220
Db 739 GGCTACAAAGTGTATGGCCGCTCCGGATGGAGAAAGAGAGATTTGTGGGGGAGTGG 798
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240
Db 799 AGCCCATTTTGTCTCTCCAGACACCGCCTTCTCTCCAAAAGATGTGTGGGTATCAGGG 858
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260
Db 859 AACCTCTGTGGGAGCGCTGGAGGAGAGAACCTTTGTTCTTATGGAAGAGGCCCGGAGGCC 918
```

261 CysValGlnValSerTyrIleValTrpPheTrpValGlyValArgGluLeuSerProGlu 280  
 919 TGTGTGCAGGTGAGCTACAAAGTCTGGTTCTGGTTGGAGTCTGAGTCCAGAA 978  
 281 GlyIleThrCysCysSerIleuLeuProSerGlyAlaGluTrpAlaArgValSerAla 300  
 979 GGAATTTACCTGTCTGCTCCCTAATTCACAGTGGCGGAGTGGGCCAGAGGTCTCCGCT 1038  
 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
 1039 GTCAAGCCACAGCTGGGAGGCTCTCAACACCTCTCTTTGTGTGCTTGGATTGAGCC 1098  
 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
 1099 TCTGCCCCCGTAGCGTGGCAGTCAGCAGCATCGCTGGGAGCAGGAGTACTGTGTACC 1158  
 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
 1159 TGGCAACCGGGGCTTGGGGAACCACTGGAGCATGTAGTGGACTGGGCTCGAGATGGGAC 1218  
 361 ProLeuGluLeuLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
 1219 CCCTTGGAGAACTCAACTGGGTGGGCTTCCCTTGGGAACTCAGTCTCTGTTTACCA 1278  
 381 GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly 400  
 1279 GGGAAATTTCACTGTCTGGGGTCCCTATCGATCATGTGACCGCAGTCTCTGCTTCAGGC 1338  
 401 LeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
 1339 TTGGCTCTGTCATCTCTCGCTGGGGTTTCAAGAGGAATTAGCACCCCTAGTGGGCCA 1398  
 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
 1399 AGCTTTTGGCAGTCCAAAGTGGGCTTCCAGGAGCCCTCCGATAGCGTGGGAGAGGTC 1458  
 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460  
 1459 CCNAGGCACAGCTTCGAGGCCACCTCACCCACTACACCTTGTGTGCAGAGTGGAACT 1518  
 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
 1519 AGCCCTCTCGCTGTGATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCTGACCTT 1578  
 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
 1579 CCTTGGGGTCCCTGTGAGCTGTGGGTGAGCAGCATCTACCATCTGCTGGACAGGCCCCCT 1638  
 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpIleValLeuProGly 520  
 1639 GGTCCCATCTCTCGGCTTCTATCCAGATATACCCCTGAGTGGGAAAGTTCTGCCAGGC 1698  
 521 IleLeuPheLeuTrpGlyLeuPheLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
 1699 ATCTATTCTTGTGGGCTTGTCTCTGTGGGTGGGCTGAGCTGAGCTGGCCACCTCTGGA 1758  
 541 ArgCysTyrHisLeuArgHisIleValLeuProArgTrpValTrpGluIleValProAsp 560  
 1759 AGTGTGTACCATCTAGGACCAAGAGTGTGGCCCTGCTGGGTCTGGGAGAAAGTTCTCGAT 1818  
 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
 1819 CTGCCCCAAGCAGTTCAGGCCAGCCCCACATGGAGCAGTACCTGAGGCCCGCCCTT 1878  
 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600  
 1879 GGGACTTGGCCATCTCTGAAGTGGAGGAGATGGAGCCCCCGCGCTTATGGAGTCTCTCC 1938  
 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluIleHisPheLeuProThr 620  
 1939 CAGCCGCCAGGCCACCGCCCGCTGACTCTGGGTATGAGAAGCAGTCTCTGCCCCACA 1998  
 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636

1999 CCTGAGGAGCTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2046  
 RESULT 5  
 US-10-342-887-1092  
 ; Sequence 1092, Application US/10342887  
 ; Publication No. US20040058340A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dai, Hongyue  
 ; APPLICANT: He, Yudong  
 ; APPLICANT: Linsley, Peter S.  
 ; APPLICANT: Mao, Mao  
 ; APPLICANT: Roberts, Christopher J.  
 ; APPLICANT: Van 't Veer, Laura Johanna  
 ; APPLICANT: Van de Vijver, Marc J.  
 ; APPLICANT: Bernards, Rene  
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
 ; FILE REFERENCE: 9301-188-999  
 ; CURRENT APPLICATION NUMBER: US/10/342,887  
 ; CURRENT FILING DATE: 2003-01-15  
 ; PRIOR APPLICATION NUMBER: 60/298,918  
 ; PRIOR FILING DATE: 2001-06-18  
 ; PRIOR APPLICATION NUMBER: 60/380,710  
 ; PRIOR FILING DATE: 2002-05-14  
 ; PRIOR APPLICATION NUMBER: 10/172,118  
 ; PRIOR FILING DATE: 2002-06-14  
 ; NUMBER OF SEQ ID NOS: 2699  
 ; SEQ ID NO 1092  
 ; LENGTH: 2663  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-342-887-1092  
 Alignment Scores:  
 Pred. No.: 8,41e-310 Length: 2663  
 Score: 3498.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 17 Gaps: 0  
 US-10-088-950A-1 (1-636) x US-10-342-887-1092 (1-2663)  
 QY 1 MetArgGlyGlyValArgGlyAlaProPheTrpLeuTrpProLeuProIleValAlaLeuLeu 20  
 DB 139 ATGCGGGGAGGAGGAGGCGCCCTTCTGGCTGTGGCGCTGCCAGCTGCCAGCTGGCGTCTG 198  
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
 DB 199 CCTCTGTGTGGTCTCTTCCAGCGGACGGCTCCCGAGGCGAGCGCGCGGCGCACTGCAG 258  
 QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60  
 DB 259 TGCTACGAGTGTGGACCTTGGCGACTTGAACCTCTCTGGGAGCCTCTTGGGAGCCG 318  
 QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
 DB 319 GGAGGCCCCCTCCAGTGTACCTCCAGAGCCCAAAAGTACCGTTCCAAACAAACCCAGACT 378  
 QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
 DB 379 GTGGCAGTGGCAGCGGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGTCT 438  
 QY 101 AspLysLeuLeuValTrpGlyThrIleValGlnProLeuTrpProValPheVal 120  
 DB 439 GACAAACTCTTGTCTGGGGCACAAGGAGCCAGCCAGCTCTCTGGCCCCCGCTCTTCG 498  
 QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 DB 499 AACCTAGAAACCAATAGAGCAACCGCCCCCGGCTGGGCGCTGACGTGACGCTTTC 558  
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160



Db 559 GAGGATGACCCCTGGAGGCCACCTGTCCATTGGGCCCCCACCCTACATGGCCATCATATA 618  
Qy 161 ValLeuileCysGlnPheHisTyArgArgCysGlnGlnAlaAlaTPrThrLeuLeuGlu 180  
Db 619 GTTCTGATCTGCCAGTTCCACTACCGAAGATGTGAGGAGGGCGCTGGACCCCTGCTGAA 678  
Qy 181 ProGluLeuYsThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
Db 679 CCGAGAGCTGAAGACCATACCCCTGACCCCTGTTGAGATCCAAGATTTGGAGCTAGCCACT 738  
Qy 201 GlyTyRlyValTyGlyArgCysArgMetGluYsGluGluAAspLeuTrpGlyGluTrp 220  
Db 739 GGCTACAAAGTGTATGGCCGTGCGGATGAGAGAAAGAGGATTTGTGGGGCGAGTGG 798  
Qy 221 SerProIleLeuSerPheGlnThrProProSerAlaProYsAspValTrpValSerGly 240  
Db 799 AGCCCCATTTTGTCTTCCAGACACCCGCTTCTGCTCCAAAGATGTGGGTATCAGGG 858  
Qy 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyPro 260  
Db 859 AACCTCTGTGGAGCGCTGGAGGAGAGAACCTTTGCTTCTATGGAAGGCCCCAGGGGCC 918  
Qy 261 CysValGlnValSerTyRlyValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
Db 919 TGTGTGAGGTGAGCTACAAAGTCTGGTCTTGGGTGTGAGGTCTGTGAGCTGAGTCCAGAA 978  
Qy 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
Db 979 GGAATTACCTGCTGCTGCTCCTTAATTCCTAGTGGGGGGGAGTGGGCCAGGGTGTCCGCT 1038  
Qy 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
Db 1039 GTCAACGCCCAAGCTGGAGCCTCTACCAACCTCTCTTTGGTCTGCTGGATTACGCC 1098  
Qy 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
Db 1099 TCTCCCCCGGTGAGCTGGAGTGGAGTCAGCAGCATCTCGGGAGCAGCGAGCTACTGGTACC 1158  
Qy 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
Db 1159 TGGCAACCGGGGCTTGGGAAACCACTGGAGCATGTAGTGACTGGGTTCGAGATGGGGAC 1218  
Qy 361 ProLeuGluYsLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
Db 1219 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTCCCTGGGAACCTCAGTGTCTGTACCA 1278  
Qy 381 GlyAsnPheThrValGlyValProTyArgIleThrValThrAlaValSerAlaSerGly 400  
Db 1279 GGGAAATTTCACTGTCGGGGTCCCTATCGAATCACTGTGACCGCAGTCTCTGTCTCAGGC 1338  
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
Db 1339 TTGGCTCTGATCTCTCGTCTGGGGTTTCAAGGAGGAATAGCACCCCTTAGTGGGGCCA 1398  
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
Db 1399 ACGTTTGGGACTCCAAAGATGCCCTCCAGGAGCCCCCGCATAGCTGGGGAGAGTTC 1458  
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyRlyThrLeuCysAlaGlnSerGlyThr 460  
Db 1459 CCAAGGACCAACGCTTCGAGGCCACCTCACCACTACACCTTGTGTGACAGAGTGAAC 1518  
Qy 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
Db 1519 AGCCCTCTCGTCTGCATGAATGTGAGTGGCAACACAGAGTGTACCCCTGCCTGACCTT 1578  
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
Db 1579 CCTTGGGGTCCCTGTGAGCTGTGGTGACGATCTACCATCGTGTGACAGGGGCCCTCCT 1638  
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
Db 1639 GGTCCCATCTCCGGCTTCTATCACCAGATAACACCCCTGAGGTGAAAGTTCTTGCCAGGC 1698

## RESULT 6

US-10-755-889-163

; Sequence 163, Application US/10755889

; Publication No. US20040171823A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB

; FILE REFERENCES: D0284 NP

; CURRENT APPLICATION NUMBER: US/10/755,889

; CURRENT FILING DATE: 2004-01-13

; PRIOR APPLICATION NUMBER: U.S. 60/440,068

; PRIOR FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: U.S. 60/469,757

; PRIOR FILING DATE: 2003-05-12

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 163

; LENGTH: 3258

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-755-889-163

Alignment Scores:

Pred. No.:	1,07e-309	Length:	3258
Score:	3498.00	Matches:	636
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-088-950A-1 (1-636) x US-10-755-889-163 (1-3258)

Qy 1 MetArgGlyArgGlyAlaProPheTrpLeuTrpProLeuProYsLeuAlaLeuLeu 20

Db 424 ATCGGGGAGGAGCGGGCGCCCTTTCTGGCTGTGGCGCTGCCAAGCTGGGGCTGCTG 483

Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

Db 484 CCTCTGTGTGGGTGCTTTTCCAGCGGACGCGTCCCGAGGCGCGCGGGCCACTGCAG 543

Qy 41 CysTyRTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 544 TGCTACGGAGTTGACCCCTTGGCGACTTGAACCTGCTCGTGGGAGGCTCTTGGGGACTG 603

Qy 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyRArgSerAsnLysThrGlnThr 80

Db 604 GGAGCCCTCCGAGTTACACCTCCAGAGCGCAAAAGTACCGTTCCCAAAACCCAGACT 663

QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
 DB 664 GTGGCAGTGGCAGCGGAGCGAGTGGTGGCCATTCTCTGGGACAGCTCACCATGCT 723  
 QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
 DB 724 GACAAACTCTTGTCTGGGGCACTAAGGAGCGGAGCGGAGCTCTCTGGGCCCCCGCTCTTCGTG 783  
 QY 121 AsnLeuGluThrClnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 DB 784 AACCTAGAAACCCAAATGAAGCAACACGCCCGGCTGGGCTGACGTGGACTTTTCC 843  
 QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160  
 DB 844 GAGGTGACCCCTGGAGGCCACTGTCCATTTGGGCCCACTACATGGCCATCTCATAA 903  
 QY 161 ValLeuLeuCysGlnPheHisTrpArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
 DB 904 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTCCAGAGCGGCGCTGGACCTGTCTGAA 963  
 QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
 DB 964 CCGAGCTGAAGACCATACCCCTGACCCCTGTGTAGATCCAAAGATTGGAGCTAGCCACT 1023  
 QY 201 GlyTrpLysValTrpGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrp 220  
 DB 1024 GGCTACAAAGTGTATGGCGCTGCCGAGTGGAGAAAGAGAGATTGTGGGGCGAGTGG 1083  
 QY 221 SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly 240  
 DB 1084 AGCCCATTTTGTCTTCCAGACACCGCTTCTGTCTCCAAAGATGTGTGGGTATCAGGG 1143  
 QY 241 AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLysAlaProGlyPro 260  
 DB 1144 AACCTCTGGGGAGCGCTGGAGAGAGAACTTGTCTTATGGAAGCGCCAGGGGCC 1203  
 QY 261 CysValGlnValSerTrpLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu 280  
 DB 1204 TGTGTGAGGTGAGTACAAAGTCTGGTCTGGTGGAGTCTGTGAGTGTGAGTCCAGAA 1263  
 QY 281 GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla 300  
 DB 1264 GGAATTAACCTGTCTGTCTCCCTAAATCCAGTGGGGCGAGTGGGCCAGGCTGTCCGCT 1323  
 QY 301 ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla 320  
 DB 1324 GTCAACGCCACAGCTGGAGGCTCTCCACCACTCTCTTGTGTCTGTGTGATTCAGGC 1383  
 QY 321 SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr 340  
 DB 1384 TCTGCCCGCTGAGCTGGCAGTACAGCATCGCTGGGACGAGCTACTGTGTGACC 1443  
 QY 341 TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp 360  
 DB 1444 TGGCAACCGGGCTGGGCAACCACTGGAGCATGTAGTGGCTGGGCTCGAGATGGGAC 1503  
 QY 361 ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro 380  
 DB 1504 CCCCTGGAGAACTCAACTGGGTGGGCTTCCCGCTGGGAACTCAGTGTCTGTGTACCA 1563  
 QY 381 GlyAsnPheThrValGlyValProTrpArgIleThrValThrAlaValSerAlaSerGly 400  
 DB 1564 GGGAAATTCATGTGGGGTCCCTATCGAATACATGTGACCGCATCTCTGTCTCAGGC 1623  
 QY 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
 DB 1624 TTGGCTCTGCATCTCTGGGGTTCAGGGAGGAAATAGCACCCCTAGTGGGGCCA 1683  
 QY 421 ThrLeuTrpArgLeuGlnPheAlaProGlyThrProAlaIleAlaTrpGlyGluVal 440  
 DB 1684 ACCGTTTGGGAGTCCAAAGATGCCCTCCAGGGACCCCGCCATAGCGTGGGGAGAGGTC 1743

QY 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTrpThrLeuCysAlaGlnSerGlyThr 460  
 DB 1744 CCAAGGCCACAGTTCGAGGGCCACCTCACCCACTACACTTGTGTGTCACAGAGTGGAAAC 1803  
 QY 461 SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu 480  
 DB 1804 AGCCCTCCGTCTGATGAATGTGAGTGGCAACACAGAGGTGTCACTGCTGCTGACCTT 1863  
 QY 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
 DB 1864 CTTTGGGTCTCTGTGAGCTGTGGGTGACGATCTACATCGCTGGACAGGGCCCTCTCT 1923  
 QY 501 GlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLysValLeuProGly 520  
 DB 1924 GGTCCCATCTCCGGCTTCTATCTACAGATAACACCTGAGGTGAAAGTTCTGCGGGC 1983  
 QY 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
 DB 1984 ATCTTATTCTTGTGGGGCTTGTCTGTGGGTGTGGCTGAGCTGGCCACCTCTTGA 2043  
 QY 541 ArgCysTrpHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
 DB 2044 AGTCTCTACCACTTAAGGACAAAGTGTGCCCCCTGGGTCTGGGAGAAAGTCTCTGAT 2103  
 QY 561 ProAlaAsnSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
 DB 2104 CTTGCAACAGCAGTTCAGGCCAGCCCCACATGGAGCAAGTACCTGAGGCCAGCCCTT 2163  
 QY 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProProValMetGluSerSer 600  
 DB 2164 GGGGACTTGTCCCATCTCTGAAAGTGGAGAGATGGAGCCCCCGGCTTATGGAGTCTCC 2223  
 QY 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTrpGluLysHisPheLeuProThr 620  
 DB 2224 CAGCCCCGCGAGGCCACCGCCCTTGCCTGCTGGGTATGAGAGCACTTCTGTGCCACA 2283  
 QY 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
 DB 2284 CTTGAGGAGTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2331

RESULT 7  
 US-09-791-497-13  
 ; Sequence 13, Application US/09791497  
 ; Publication No. US20030008343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Timans, Jacqueline C.  
 ; APPLICANT: Kastelein, Robert A.  
 ; APPLICANT: Bazan, J. Fernando  
 ; APPLICANT: Pflanz, Stefan  
 ; FILE REFERENCE: DX01040K2  
 ; CURRENT APPLICATION NUMBER: US/09/791,497  
 ; CURRENT FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: 09/627,897  
 ; PRIOR FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: 60/146,581  
 ; PRIOR FILING DATE: 1999-07-30  
 ; PRIOR APPLICATION NUMBER: 60/147,763  
 ; PRIOR FILING DATE: 1999-08-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 13  
 ; LENGTH: 2628  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (112) .. (2022)  
 US-09-791-497-13

Alignment Scores: 1,928-309 Length: 2628  
 Pred. No.: 3494.00 Matches: 635  
 Score:

Percent Similarity:	99.84%	Conservative:	0
Best Local Similarity:	99.84%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	10	Gaps:	0
US-10-088-950A-1 (1-636) x US-09-791-497-13 (1-2628)			
Qy	1	MetArgGlyGlyArgGlyAlaProPheThrLeuTrpProLeuProLyLeuAlaLeuLeu	20
Db	112	ATGCGGGAGGACGCGGGCGGCCCTTCTTGCGTGTGGCGCTGCCCCAAGCTGGCGGCTGCTG	171
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlnYSerAlaGlyProLeuGln	40
Db	172	CCTCTGTTGGGGTGTCTTTTCCAGCGGACGGGTCCCAAGGCGAGCGCGGGCCACTGCGAG	231
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	232	TGCTACGGAGTTTGACCTTGCGGCATTTGAACATGCTCTGGAGCCCTCTTTGGGACCTG	291
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	292	GGAGCCCCCTCCGAGTTTACACCTCCAGAGCCAAAAGTACCGTTCCAACAAAACCCAGACT	351
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaLeProArgGluGlnLeuThrMetSer	100
Db	352	GTGGCACTGGCAGCGGACGAGCTGGGTGGCCATTCTCCGGGAACAGCTCACCATTGCT	411
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal	120
Db	412	GACAAATCTCTTGTCTGGGCACATAAGCAGCCAGCCCTCTCTGGCCCCCGCTCTTCGTG	471
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	472	AACCTAGAAACCCAAATGAAGCCAAAACGCCCTCCCGCTGGGCCCTGAGCTGGACTTTTCC	531
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	532	GAGGATGACCCCTCGAGGCGCACATGTCTCATTTGGGCCCCACCCTACATAGCCCATCTATAAA	591
Qy	161	ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu	180
Db	592	GTTCTGATGTGCCAGTTTCCACTACCGAAGATGTGAGGAGGCGGCTGAGCCCTCGTGAA	651
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	652	CCGGAGCTGAAGACCATACCCCTGACCCCTGTTCAGATCCAGATTTGGAGCTAGCCACT	711
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTrpGlyLysTrp	220
Db	712	GGCTACAAAGTGTATGGCCGCTGCCGATGGAGAAAGAGGATTTGTGGCGCGAGTGG	771
Qy	221	SerProfileLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	772	AGCCCCAATTTGTCTTCCAGACACCCGCTTCTGCTCCAAAGATGTGTGGGTATCAAGG	831
Qy	241	AsnLeuCysGlyThrProGlyGlyGluProLeuLeuTrpLysAlaProGlyPro	260
Db	832	AACCTCTGTGGAGCCCTGGAGGAGAGAACCTTTGTCTTATUGAAGGCCCCAGGGCCC	891
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	892	TGTGTGAGGTGAGCTACAAAGTCTGGTCTCTGGGTGGAGGTCTGAGCTGAGTCCAGAA	951
Qy	281	GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
Db	952	GGAAATACCTGCTGCTCTCCCTAAATTTCCACAGTGGGCGGAGTGGGCGCTGCGCT	1011
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	1012	GTCAACGCCACAGCTGGGAGCCTCTCACCAACCTCTCTTTGGTCTGCTTGGATTCAGCC	1071
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340

; APPLICANT: Cheung, Jeanne  
 ; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS  
 ; FILE REFERENCE: DX01040K3  
 ; CURRENT APPLICATION NUMBER: US/10/000,776  
 ; CURRENT FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: 09/791,497  
 ; PRIOR FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: 09/627,897  
 ; PRIOR FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: 60/146,581  
 ; PRIOR FILING DATE: 1999-07-30  
 ; PRIOR APPLICATION NUMBER: 60/147,763  
 ; PRIOR FILING DATE: 1999-08-06  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 11  
 ; LENGTH: 2628  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (112)..(2019)  
 ; OTHER INFORMATION:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2433)..(2433)  
 ; OTHER INFORMATION: Unidentified base.  
 ; US-10-000-776-11

Alignment Scores:  
 Pred. No.: 1,92e-309 Length: 2628  
 Score: 3494.00 Matches: 635  
 Percent Similarity: 99.84% Conservative: 0  
 Best Local Similarity: 99.84% Mismatches: 1  
 Query Match: 99.89% Indels: 0  
 DB: 13 Gaps: 0

US-10-088-950A-1 (1-636) x US-10-000-776-11 (1-2628)

QY	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
DB	652	CCGGAGCTGAAGACCATACCTCCCTGACCCCTGTTGAGATCCAGATTTCGAGTACCCACT	711
QY	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluAspLeuTyrGlyGluTyr	220
DB	712	GGCTACAAAGTGTATGGCGCTGCGGATCGAGAGAGAGAGATTTCGCGCGCAGTGG	771
QY	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTyrValSerGly	240
DB	772	AGCCCCATTTTGTCTCCACACACCGCTTCTGCTCAAAAGATGTGTGGGTATCAGG	831
QY	241	AsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTyrLysAlaProGlyPro	260
DB	832	AACTCTGTGGAGCGCTGGAGGAGGAACTTTGCTTCTATGGAAGCCCGAGGCC	891
QY	261	CysValGlnValSerTyrLysValTyrPheTyrValGlyArgGluLeuSerProGlu	280
DB	892	TGTGTGAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGTCTGTGAGCTGAGTCCAGAA	951
QY	281	GlyIleThrCysCysSerLeuIleProSerGlyAlaGluTyrAlaArgValSerAla	300
DB	952	GGATTACCTGCTGCTCTCCCTAATCCAGTGGGCGGAGTGGGCGAGGTGTCCCT	1011
QY	301	ValAsnAlaThrSerTyrGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
DB	1012	GTCAACGCCACACAGCTGGAGGCTCTCACCAACCTCTCTTGGTCTGTGGATTGAGCC	1071
QY	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
DB	1072	TCTGCCCCCGCTAGCGTGGAGTACAGCAGTCTGGGAGCAGCAGCTACTGTGAGCC	1131
QY	341	TyrGlnProGlyProGlyGluProLeuGluHisValValAspTyrAlaArgAspGlyAsp	360
DB	1132	TGGCAACCGGGGCGCTGGGGAACCACTGGAGCATGTAGTGGACTGGGCTGAGATGGGAC	1191
QY	361	ProLeuGluLysLeuAsnTyrValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380
DB	1192	CCCCCTGGAGAACTCAACTGGGTCCGGCTTCCCCCTGGGAACCTCAGTGTCTGTACCA	1251
QY	381	GlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGly	400
DB	1252	GGGAATTTCACTGTGGGGTCCCTATCGAATCACTGACCGCAGTCTCTGCTTTCAGGC	1311
QY	401	LeuAlaSerAlaSerSerValTyrGlyPheArgGluGluLeuAlaProLeuValGlyPro	420
DB	1312	TTGGCCTCTGCATCTCTCGTCTGGGGGTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA	1371
QY	421	ThrLeuTyrArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTyrGlyGluVal	440
DB	1372	AGCTTTGGGACTCCAGATGCCCCCTCCAGGGACCCCGCCCATAGCTGGGGAGAGGTC	1431
QY	441	ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr	460
DB	1432	CCAGGACCAAGCTTCGAGGCGCACCTCACTCCACTACACCTGTGTGTCACAGAGTGAACC	1491
QY	461	SerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeu	480
DB	1492	AGCCCCCTCGTGTGATGAATGTAGTGGGACACACAGAGGTGTACCTGTCTGACCTT	1551
QY	481	ProTyrGlyProCysGluLeuTyrValThrAlaSerThrIleAlaGlyGlnGlyProPro	500
DB	1552	CCTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGAGGCGCCCTCT	1611
QY	501	GlyProIleLeuArgLeuHisLeuProAspLeuThrLeuArgTyrPlysValLeuProGly	520
DB	1612	GGTCCCATCTCCGCTTCTATCTACAGATAACCTCAGGTGGAAGATTCTGCGGGGC	1671
QY	521	IleLeuPheLeuTyrGlyPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly	540
DB	1672	ATCCTATTCTTGTGGGGCTTGTCTGTGGGGGTGTGGCTGAGCTGAGCCACCTCTGGA	1731

Qy 541 ArgCysTyrHisLeuArgHisLeuValLeuProArgTrpValTrpGluLysValProAsp 560  
Db 1732 AGGTGCTACCACTAAGGCACAAAGTGTGCTGCCCGCTGGGTCTGGGAGAAAGTTCTCTGAT 1791  
Qy 561 ProAlaAsnSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
Db 1792 CCTGCCAACAGCAGTTTTCAGGCCAGCCACATGAGCAAGTACCTGAGAGCCACGCCCTT 1851  
Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600  
Db 1852 GGGGACTTGGCCATCTGCTGAGTGTGAGGAGATGAGAGCCCGCCGCTTATGGAGTCTCTCC 1911  
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
Db 1912 CAGCCCGCCAGGCGCCCGCCCTTGACTCTGGGTATGAGAAGCATTCTCTGCCACA 1971  
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
Db 1972 CCTGAGGAGCTGGGCCCTTCTGGGGCCCCCAGGCGCCAGAGTTCTGGCC 2019

## RESULT 9

US-10-777-790-11  
; Sequence 11, Application US/10777790  
; Publication No. US20040198955A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Pflanz, Stefan K.-H.  
; APPLICANT: Kaetelein, Robert A.  
; APPLICANT: Bazan, Jose F.  
; APPLICANT: Rennick, Donna  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Cheung, Jeanne  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS  
; FILE REFERENCE: DX01040K3  
; CURRENT APPLICATION NUMBER: US/10/777,790  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/10/000,776  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 03/791,497  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 09/627,897  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,581  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 60/147,763  
; PRIOR FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 2628  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (112)..(2019)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2433)..(2433)  
; OTHER INFORMATION: Unidentified base.  
US-10-777-790-11

## Alignment Scores:

Pred. No.:	1.92e-309	Length:	2628
Score:	3494.00	Matches:	635
Percent Similarity:	99.84%	Conservative:	0
Best Local Similarity:	99.84%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	18	Gaps:	0

US-10-088-950A-1 (1-636) x US-10-777-790-11 (1-2628)

Qy 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLysLeuAlaLeuLeu 20

Db	112	ATGCGGGAGCGAGGGCGGCCCTTTCTGGCTGTGGCGCTGCCAAGCTGGCGCTCTG	171
Qy	21	ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlnGlySerAlaGlyProLeuGln	40
Db	172	CCTCTGTGTGGGTGCTTTTCCAGCGGACGCGTCCCAGGGCAGCGCGGGCCACTCGAG	231
Qy	41	CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu	60
Db	232	TGCTACGAGTTGGACCCCTTTGGGCGACTTCAACTGCTCGTGGGAGCCTCTTTGGGACCTG	291
Qy	61	GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr	80
Db	292	GGAGCCCCCTCCGAGTTTACACCTCCAGAGCAAAAGTACCGTTCCAAACAAACCCAGACT	351
Qy	81	ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuLeuMetSer	100
Db	352	GTGGCAGTGGCAGCGGACGAGCTGGGTGGCCATTCTCGGGAACAGCTCACCATGTCT	411
Qy	101	AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal	120
Db	412	GACAAACTCTCTGTGGGSCACTAAGGCAGGCGAGCCTCTCTGGCCCCCGTCTTCGTG	471
Qy	121	AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer	140
Db	472	AACCTAGAAACCCCAATGAAGCCAAACGCCCGCGCTGGGCGCTGACGTGGACTTTTCC	531
Qy	141	GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys	160
Db	532	GAGGATGACCCCTGGAGGCCACTGTCCATTGGGCGCCACTACATGCCCATCTCTCAAAA	591
Qy	161	ValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAlaIleTrpThrLeuLeuGlu	180
Db	592	GTCTGTCTGCCAGTTCCACTACCGAAGATGTCCAGAGCGCGCTGGACCTCTCGAA	651
Qy	181	ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr	200
Db	652	CCGGAGCTGAAGACCATACCCCTGACCCCTGTGTGAGATCCAAAGATTTGGAGTAGCCACT	711
Qy	201	GlyTyrLysValTyrGlyArgCysArgMetGluLysGluLeuAspLeuTrpGlyGluTrp	220
Db	712	GGCTACAAAGTGTATGGCGCTCCCGGATGAGAAAGAGAGATTTGTGGGCGAGTGG	771
Qy	221	SerProIleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGly	240
Db	772	AGCCCCATTTGTCTCTCCAGACACCGCCCTTCTGCTCCAAAAGATGTGTGGGTATCAGGG	831
Qy	241	AsnLeuCysGlyThrProGlyGlyGluProLeuLeuLeuTrpLysAlaProGlyPro	260
Db	832	AACCTCTGTGGGACCGCTGGAGGAGAGAACCTTTGCTTCTATGGAAGGCCCCAGGGGCC	891
Qy	261	CysValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGlu	280
Db	892	TGTGTGCAGGTGAGCTACAAAGTCTGGTCTGGGTGGAGGTCTGTGAGGTCCAGAA	951
Qy	281	GlyIleThrCysCysCysSerLeuIleProSerGlyAlaGluTrpAlaArgValSerAla	300
Db	952	GGAAATTACCTGTCTGTCTCCCTAAATTCAGTGGGGCGGAGTGGGCGAGGGTGTCCGCT	1011
Qy	301	ValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAla	320
Db	1012	GTCAACGCCACAAGCTGGGAGCCTCTCAACCACTCTCTTTGCTGTCTTGGATTACGCC	1071
Qy	321	SerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThr	340
Db	1072	TCTGCCCGCCGTAGCTGGCAGTACAGCAGCATCGCTGGGAGCAGGAGTACTTGGTGACC	1131
Qy	341	TrpGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAsp	360
Db	1132	TGGCAACCGGGGCTGGGGAACCATCTGGAGCATGTAGTGGACTGGGCTCGAGATGGGGAC	1191
Qy	361	ProLeuGluLysLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuPro	380

Db 1192 CCCCTGGAGAACTCAACTGGGTCCGGCTTCCCTTGGGAACCTCAGTCTCTGTACCA 1251  
Qy 381 GlyAsnPhThValGlyValProTyrArgIleThrValThAlaValSerAlaSerGly 400  
Db 1252 GGGAAATTCACCTGTCCGGGTCCCTATCAATCACTGTACCGCAGTCTCTGCTTACGCG 1311  
Qy 401 LeuAlaSerAlaSerValTrpGlyPheArgGluGluLeuAlaProLeuValGlyPro 420  
Db 1312 TTGGCCCTTGCATCCCTCCGTCTGGGGTTTCAGGGAGGAATTAGCACCCCTAGTGGGGCCA 1371  
Qy 421 ThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAlaTrpGlyGluVal 440  
Db 1372 AGCTTTGGCGACTCAAGATGCCCTCCAGGGACCCCGCCATAGCGTGGGGAGAGGTC 1431  
Qy 441 ProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThr 460  
Db 1432 CCAAGGCACAGCTTCAGGCCACCTCACCCACTACACCTTGTGTGCACAGAGTGGAAAC 1491  
Qy 461 SerProSerValCysMetAenValSerGlyAenThrGlnSerValThrLeuProAspLeu 480  
Db 1492 AGCCCTCCGTCTGCATGAATGTAGTGGCAACACACAGAGTGTACCCCTGCTGACCTT 1551  
Qy 481 ProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProPro 500  
Db 1552 CCTTGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGACAGGGCCCTCCT 1611  
Qy 501 GlyProIleLeuArgLeuHisLeuProAspAenThrLeuArgTrpLysValLeuProGly 520  
Db 1612 GGTCCCATCCTCCGGCTTCATCTACCAAGATAACACCCCTGAGGTGGAAATTCCTGGGCG 1671  
Qy 521 IleLeuPheLeuTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGly 540  
Db 1672 ATCCTATTCTTGGGGCTTGTTCCTTGTGGGTGTGGCTGAGCCCTGGCCACCTCTGA 1731  
Qy 541 ArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAsp 560  
Db 1732 AGTGTCTACCACTAAGGCACAAAGTGTGCCCGCTGGGTCTGGGAGAAAGTTCCTGAT 1791  
Qy 561 ProAlaAenSerSerSerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeu 580  
Db 1792 CTTGCCAACAAGCAAGTTCAGGCCAGCCCCACATGAGCAAGTACCTGAGGCCAGGCCCTT 1851  
Qy 581 GlyAspLeuProIleLeuGluValGluGluMetGluProProValMetGluSerSer 600  
Db 1852 GGGGACTTGGCCATCTCGAGTGGAGAGATGAGCCCCCGCGGTATGGAGTCTCTCC 1911  
Qy 601 GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThr 620  
Db 1912 CAGCCCGCCAGGCCACCGCCCGCTTGACTCTGGGTATGAGAAGCACTTCTCTGCCACA 1971  
Qy 621 ProGluGluLeuGlyLeuLeuGlyProProArgProGlnValLeuAla 636  
Db 1972 CCTGAGAGAGTGGGCTTCTGGGGCCCCCAGGCCACAGGTTCTGGCC 2019

## RESULT 10

US-10-663-158-4

; Sequence 4, Application US/10663158

; Publication No. US20040234522A1

; GENERAL INFORMATION:

; APPLICANT: Desauvage, Frederic

; APPLICANT: Grewal, Iqbal

; APPLICANT: Gurney, Austin L.

; TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCCR

; FILE REFERENCE: 11669.123USC1

; CURRENT APPLICATION NUMBER: US/10/663,158

; CURRENT FILING DATE: 2003-09-15

; PRIORITY APPLICATION NUMBER: US 09/692,504

; PRIORITY FILING DATE: 2000-10-18

; PRIORITY APPLICATION NUMBER: US 60/160,542

; PRIORITY FILING DATE: 1999-10-20

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 2005

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-663-158-4

## Alignment Scores:

Pred. No.:	5,95e-177	Length:	2005
Score:	2044.00	Matches:	388
Percent Similarity:	72.55%	Conservative:	61
Best Local Similarity:	62.78%	Mismatches:	161
Query Match:	58.43%	Indels:	8
DB:	18	Gaps:	3

US-10-088-950A-1 (1-636) x US-10-663-158-4 (1-2005)

Qy 14 LeuProLysLeuAlaLeuLeuProLeuLeuTrpValLeuPheGlnArgThrArgProGln 33  
Db 45 CTCAGCGCTTGGAGCTTCTCTGCTGCTGATGTGCTGCTGGGACGCGGCCCCAC 104  
Qy 34 GlySerAlaGlyProLeuGlnCysTyrGlyValGlyProLeuGlyAspLeuAsnCysSer 53  
Db 105 GGCAGTCCAGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 164  
Qy 54 TrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyr 73  
Db 165 TGGGAACCTTTGGGCGACTCGAGACTCCACTGTGCTGTATCACAGAGTCAGAAATAC 224  
Qy 74 ArgSerAenLysThrGlnThrValAlaValAlaAlaGlyArgSerTrpValAlaIlePro 93  
Db 225 CATCCCAATAGACTCTGGAGGTGAAGGTGCTTCCAAACAAAGTTGGGTGACCAATCCC 284  
Qy 94 ArgGluGlnLeuThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnPro 113  
Db 285 CGGGAACAGTTCACCATGGCTGACAACTCTCATCTGGGGGACACAAAAGGAGCGCT 344  
Qy 114 LeuTrpProProValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeu 133  
Db 345 CTGTGCTCTCTGCTCTGTGAACCTGGAGACCCCAATGAAGCCACAGACACACCTCAGATC 404  
Qy 134 GlyProAspValAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaPro 153  
Db 405 TTCTCTCAAGTGGATATTTCTGAGGAAGCAACCTTGGAGGCCACTGTGAGTGGGGCGCG 464  
Qy 154 ProThrTrpProSerHisLysValLeuIleCysGlnPheHisTyrArgArgCysGlnGlu 173  
Db 465 CCCGTGTGGCCACCCGACAAAGCTCTCACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 524  
Qy 174 AlaAlaTrpThrLeuLeuGluProGluLeuLysThrIleProLeuThrProValGluIle 193  
Db 525 GAAGCATGGACCCGCTGGAGCCCGCCAGCTGAAGACAGATGGGCTGACTCTCTTGGAGATG 584  
Qy 194 GlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213  
Db 585 CAGAACCTGGAAACCTGGGACCTGCTACAGGTGTCTGGCCGCTGCGAGGTGGAGAACGGA 644  
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaPro 233  
Db 645 TATCCA--TGGGGCGAGTGGAGTTTGGCCCTGTCTCTCCAGACGCCATCTCTAGATCTCT 701  
Qy 234 LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeu 253  
Db 702 GAAGATGTGGGTATCGGGGACCGCTCTGTGAACACTTCTGGCAAAACGGGACGCCCTGCTT 761  
Qy 254 LeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrpValGly 273  
Db 762 GTCTGGAAGGCCCAAGACTTGTGTGAGGTGACTTACACAGTCTGGTTTGGGGCTGGA 821  
Qy 274 GlyArgGluLeuSerProGluGlyLeuThrCysCysCysSerLeuIleProSerGlyAla 293  
Db 822 GATATTACTACAACTCAAGAGAGGTCCCGTCTGCAAGTCCCTGCTCTCTGCTGCTGATG 881  
Qy 294 GluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrProLeuSer 313



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Db 882 GAGTGGGCTGGTCTCTCTCTGGCAACAGCAGCTGGGTGCTCCACCAACCTGTCT 941
Qy 314 LeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerIleAlaGly 333
Db 942 CTGGTGTCTGGCTCCAGATCTGCCCTCTGACGTGGAGTGAGCAGTGTGATGGG 1001
Qy 334 SerThrGluLeuValThrTrpGlnProGlyProGlyGluProLeuGluHisValVal 353
Db 1002 AGCCACAGGATTAAGGTGACCTGGAAACAGAGGACCAAGAAACCAATTGGAGTAGTGTGGTG 1061
Qy 354 AspTrpAlaArgAspGlyAspProLeuGluLysLeuSerTrpValArgLeuProProGly 373
Db 1062 GACTGGGCTCAAGATGGTGACGCTGGCAAGCTCAACTGGACCCGCTCTCCCCCTGGGA 1121
Qy 374 AsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVal 393
Db 1122 AACCTCAGCACATTTTACCAAGGGAGTTCAAGAGGGGTCCCTATCGAATTACAGTG 1181
Qy 394 ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluGlu 413
Db 1182 ACTGCAGTATCTCTGGAGGATAGTCTGCACCCCTCAGTTTGGGGATTTCAGAGAGGAG 1241
Qy 414 LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro 433
Db 1242 TTAGTACCCCTTGTGGCCAGAGTTCCTGGGAGCTTCCAGATGACCCCCAGGAGACCT 1301
Qy 434 AlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrThr 453
Db 1302 GTTGTAGCTGGGAGAGTACCAAGACACACAGCTCAGAGCCAGGCTACTCTACATACC 1361
Qy 454 LeuCysAlaGlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGln 473
Db 1362 TTCTGCATACAGACAGAGGCTCTCCACTGTCTGCAGGAACGTGAGCAGTCAAAACCCAG 1421
Qy 474 SerValThrLeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThr 493
Db 1422 ACTGCCACTCTGCCAACCTTCTACTCGGGTTCCTTCAAGTGTGGGTGACGGTGTCCACC 1481
Qy 494 IleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeu 513
Db 1482 GTTCAGAGCAGGCGCCACCTGGTCCCGACCTTTCACCTTACCTACCAAGATATAGGATC 1541
Qy 514 ArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuGlyCysGly 533
Db 1542 AGGTGGAAGAGCTCGCCCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1601
Qy 534 LeuSerLeuAlaThrSer-----GlyArgCysTyrHisLeuArgHisLysVal 549
Db 1602 CTGAGCTGGCCAGTACAGGTGCTACAGCCAGGTGCTTACACTGGCCAGCACAGTTG 1661
Qy 550 LeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerGlyGlnPro 569
Db 1662 CTTCCTCCAGTGGATCTGGAGAGGTTCTGTATCTCTGCCAACAGCAATTTCTGGGCAACCT 1721
Qy 570 HisMetGluGlnValProGluAlaGlnProLeuGlyAspLeuProIleLeuGluValGlu 589
Db 1722 TACATCAAGGAGGTGAGCTGCCCAACCGCCCAAGGACGACCATCTCTGGAGTGGAG 1781
Qy 590 GluMetGluProProProValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu 609
Db 1782 GAAGTGGAGCTACAGCTGTGTGGAGTCC-----CCTAAAGCTCTGCCCCGATT 1832
Qy 610 AspSerGlyTyrGluLysHisPheLeuProThrProGluGluLeuGlyLeuLeu 627
Db 1833 TACTCTGGGTATGAGAAACACTTCTGCCCAACAGGAGGCTGGGCCCTTCTA 1886
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## RESULT 11

US-10-370-715B-67

; Sequence 67, Application US/10370715B

; Publication No. US20040258678A1

; GENERAL INFORMATION:

; Patin Docket Preview

; APPLICANT: BODARY, SARAH C.

```
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: PI94891-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 67
; LENGTH: 4040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-370-715B-67
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Alignment Scores:
Pred. No.: 1,58e-24 Length: 4040
Score: 381.50 Matches: 189
Percent Similarity: 38.18% Conservative: 92
Best Local Similarity: 25.68% Mismatches: 285
Query Match: 10.91% Indels: 172
DB: 18 Gaps: 35
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US-10-088-950A-1 (1-636) x US-10-370-715B-67 (1-4040)

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Qy 12 TrpProLeuProLysLeuAla-Leu-----LeuProLeuLeuTrpValLeuPhe----- 27
Db 883 TGGCCACTCCTCAATTCTCAAGTCACAGGTCTTCCCTTGGTACAACTTGTGTGTG 942
Qy 27 ----- 27
Db 943 CAAACTGGCTGTATCAATAGTATGAAATTCAAATATGTGGACAGAGATCTTCGTGG 1002
Qy 28 ----GlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCysTyrGlyValGlyPr 46
Db 1003 TGTGTCTCCAGACAGCTCAAAAT-----TTATCTGCTATACAGAGGGAGA 1050
Qy 46 oLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAsp----- 59
Db 1051 ACAGGGAGCTGTGGCTGCACCTGGGAAAGAGGACGAGACACCCACTTATACACTGAGTA 1110
Qy 60 -----LeuGlyAlaProSerGluLeuHisLeuGlnSerGln----- 71
Db 1111 TACTCTACAGCTAAGTGGACCAAAAAATTTAACTGGCAGAACATGTATAAGACATTTA 1170
Qy 72 -----LysTyrArgSerAsnLysTh 78
Db 1171 TTGTGACTATTGGACTTTTGGATCAACCTCACCCCTGATCACTCAATCCAATTTTAC 1230
Qy 78 rGlnThrVal---AlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLe 97
Db 1231 AGCCAAGGTACTGTCTCAATAGTCTTGGAGGCTCTCTTCACTTCCA---TCCACATT 1287
Qy 97 uThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProPr 117
Db 1288 CACATTCTTGGACATAGTG-----AGGCCTCTT---CTCC 1320
Qy 117 oValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspVa 137
Db 1321 GTGGGACATTAGAAATCAATTTCAA---AAGGCTTCGGTGGAGCAGA----- 1363
Qy 137 lAspPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpPr 157
Db 1364 -----TGTACCCCTTATTGGAGA-----GA 1383
Qy 157 oSerHisLysValLeuLleCysGlnPheHisTyrArgArgCysGlnGluAlaTrpTh 177
Db 1384 TGAGGGAGCTGTGTACTGCTTAATCGACTCAGATATCGGCCCCAGTAACAGCAGGCTCTGGAA 1443
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QY 177 rLeuLeuGluProGluLeuLysThrIleProLeuThrProVal-----GluIle 193
Db 1444 PATG-----GTTAATGTTACAAAGGCCAAAGGAGACATGATTT 1482
QY 193 eGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysG1 213
Db 1483 GCTGGATCTGAAACCATTTACAGAAATATGAATTTCCAGATTTCTCTTAAGCTACATCTTTA 1542
QY 213 uGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPro-----Pr 230
Db 1543 TAAGGAAGTTGGAGTATGAGTGAATCATTTGAGAGCACAACACACAGGAAGAGGCC 1602
QY 230 oSerAlaProLysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluG1 250
Db 1603 TACTGGGATGTTAGATGTTCTGTACATGAACCGCACATTTGACTAC---AGTAGACAACA 1659
QY 250 uProLeuLeuLeuTrpLys-----AlaProGlyProCysValGlnVa 264
Db 1660 GATTTCTCTTTCTGGAAGAACTGAGTGTCTCAGAGGCGACAGGAAATTTCTCCACTA 1719
QY 264 lSerTyrLysValTrpPheTrpValGlyArgGluLeuSerProGlu-----GlyIle 282
Db 1720 TCAGGTGACCTTCAGAGCTGACAGGAGGAGGAAAGCCATGACACAGAACATCACAGGACA 1779
QY 282 eThrCysCysSerLeuLeuLeuProSerGlyAlaGluTrpAla---ArgValSerAlaVa 301
Db 1780 CACCTCTCGACACACATCTTCTAGAACCGGAAATGGCTGTGTGTCTGTGCGACG 1839
QY 301 lAsnAla-----ThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSe 319
Db 1840 AAATTTAAAGGAGCTTCTGCGCACTCGTATTACATAATCAACCTGTGTGGCAGG 1899
QY 319 rAlaSerAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuVa 339
Db 1900 GTTGCTGCTCTCTCGCAGGTCTCTGCAAACTCA---GAGGCGATGAGCAACATCTGTGT 1956
QY 339 lThrTrpGlnPro-----GlyProGlyGluProLeuGluHisValValAspTrpAl 356
Db 1957 GACTTGGCAGCTCCCAAGGAAAGATCTCTGCTTCAGGATGAGTGTGTGGAATGGAG 2016
QY 356 aArg-----AspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProG1 373
Db 2017 AGACCTCATCCAGGGGTGACACACAGGTCCCTCTAAACTGGCTACGGAGTGCACCTTA 2076
QY 373 yAsnLeuSerAlaLeuLeuProGlyAsnPheThrValGlyValProTyrArgIleThrVa 393
Db 2077 CAATGTGTCTGCTGCTGATTTTCAGAGAACATAAAATCCATCTGTTATGAATTCGTGT 2136
QY 393 lThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluG1 413
Db 2137 GTATGCACTCTCAGGGAT---CAAGGAGGATGCGAGTCCATCTCGGTAACTTAAGCA 2193
QY 413 uLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPr 433
Db 2194 CAAGACCACTGAGTGGCCCCCAATTAATGCCATCACAGAG---GAAAGGGAGGACAT 2250
QY 433 oAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrTh 453
Db 2251 TTTAATTTTCATGGAACAGACATCCAGTCCAGAGCAAAATGGGCTGCTCTCCATATAG 2310
QY 453 rLeuCys-----AlaGlnSerGlyThrSerProSerValCys-----MetAs 467
Db 2311 GATATCTGGAAGAACGGAGCTCCAACTCCAGCTCAGCTGTGTGAAATTCCTACAG 2370
QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487
Db 2371 AGTCTCCCAAAATTCATATCCATCAATAAACAGCGCTGAG---CCCCAGTGACATATGCTCT 2427
QY 487 utrPValThrAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHi 507
Db 2428 GTGGATGACAGCTCTGACAGCTGTGTGTGTAAGTTCCTCCACGGAATGAGAGGGAATTTTG 2487
QY 507 sLeuProAspAsnThr-LeuArgTrpTrpLysValLeuPro-----GlyIleLeuPheL 524

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Db 2488 TCTGCAAGGTAAAGCCAATTTGGATGGCGTTTGTGGCACCACCAAGCATTTTGCATTGCTATCAT 2547
QY 524 euTrpGlyLeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrH 544
Db 2548 CATGGTGGGCAATTT-----TCTCAACGCGATTACTTCCAGCAAAAAGGTGTTGT 2595
QY 544 iLeuArgHisLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnS 564
Db 2596 T-CTCTAGCAGCGCTCAGACCTCAGTGTGTAGCAGAGAAATTCAGATCCAGCAATA 2654
QY 564 erSerSerGlyGlnProHis-----MetGluGlnValProGluAlaGlnP 579
Db 2655 GCATTTGGCTAAGAAATATATCCATTTGCAGAGGAGAGACACAGCTGCCCTTTGGACAGCG 2714
QY 579 roLeuGlyAspLeuProIleLeuGluValGluGluMetGluProProPro-----595
Db 2715 TCCTGATAGATGGCCACGCTGAA-----GATCTGAAACGCTGGTTCATCA 2762
QY 596 -----ValMetGluSerSerGlnProAlaGlnAlaThrAlaProLeu-----609
Db 2763 GTGAGTCTCTTCA-TCAAGTGACCCCGAGTTTTCAGACATCCCCCTGCTCCAACCTGGCCA 2821
QY 610 -----AspSerGlyTyr-GluLysHisPheLeuProThrPro 621
Db 2822 CAAAGGGAAGAAATCCAAAGGTTCATCAGGCTCTGAGAGAAAGACATGATGCACAGTGCC 2881
QY 622 GluGluLeuGlyLeuLeuGlyProProArgProGlnValLeu 635
Db 2882 TCA-----AGCCCAACCACTCCAAAGAGCTCTC 2908

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RESULT 12

US-10-398-666-11

Sequence 11, Application US/10398666

Publication No: US20040073021A1

GENERAL INFORMATION:

APPLICANT: BIOTECHNOLOGY RESEARCH AND DEVELOPMENT CORPORATION

TITLE OF INVENTION: CLONING AND SEQUENCING OF THE PORCINE INTERLEUKIN-12

TITLE OF INVENTION: RECEPTOR BETA-1 AND BETA-2 CHAINS

FILE REFERENCE: 21419/92796

CURRENT APPLICATION NUMBER: US/10/398,666

CURRENT FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 11

LENGTH: 4023

TYPE: DNA

ORGANISM: Porcine sp.

FEATURE:

NAME/KEY: CDS

LOCATION: (230)..(2812)

US-10-398-666-11

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Best Local Similarity:	Mismatches:	Indels:	Query Match:	Gaps:
6-55e-20	4023	331.00	174	86	37.63%	263	170	9.46%	35

US-10-088-950A-1 (1-636) x US-10-398-666-11 (1-4023)

QY 31 ArgProGlnGlySerAlaGlyProLeuGlnCysTyrGlyValGlyProLeuGlyAspLeu 50

Db 605 CAGCTCTCAAAAC-----GTATCTTGTATGCAAGGAGAGACGTGGGACAGTG 652

QY 51 AsnCysSerTrpGluProLeuGlyAsp-----LeuGlyAlaProSerGluLeuHisLeu 68

Db 653 GCTGTCAGCTGGACAGACAGACGATACCCATCTATATCTATATCTTACAAATTA 712

QY 69 -GlnSerGlnLysTyrArgSerAsnLysThrGlnThrValAlaValAlaAlaGlyArgSe 88

Db	713	AATGACCAAAA-----ATTTAACTTGGCAGAAG	742
Qy	88	rTrpValaIaIeProArgGluGlnLeuThrMetSerAspLysLeuLeuVal-----Tr	106
Db	743	CAATGTAGCGATT-----ATTATGTGACTCTTTG	772
Qy	106	pGlyThrLysAlaGlyGlnProLeuTrpProValPheValAsnLeuGluThrGlnMe	126
Db	773	GACCTTGGAAATCAACCTACCCCTG-----AATCACCTGAATCTAGTTACACAG--	821
Qy	126	tLysProAsnAlaProArgLeuGlyProAspVal-----	137
Db	822	-----CCAGGTTACTGCCCATCAATAGTCTAGGGACTGGCTCTTCATATTCCCA	868
Qy	138	-----AspPheSerGluAspAs	143
Db	869	TGCACATTTCACATTTGGATGTAGTAGGGCTCTTCTCCGTGGGACATCAGAATCAAA	928
Qy	143	pProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHis---LysValle	162
Db	929	TGT-GTAAATGCCCTCCGTGAGACACATGTACCTCCAATGGAGAGATGAGGGGCTAGTGC	987
Qy	162	uileCysGlnPheHisTyzArgGlyGlnGluAlaalaalrphrLeuLeuGluProG	182
Db	988	GCTTAATCGACTAGATACCGGCTGTTTACAGCAGATCTCTGGAAATATGGTTAAT-----	1042
Qy	182	uLeuLysThrIleProLeuThrProValGluileGlnAspLeuGluLeuAlaThrGlyTy	202
Db	1043	----GCTACAAATGCCAAGGAGACATGATTGGTGGATCTGAACCTTTACAGAATA	1098
Qy	202	rLysValTyGlyArgCysArgMetGluLysGluGluAspLeuTrpGlyGluTrpSerPr	222
Db	1099	TGAATTTTCAGATTTCTCTAAGCCACATCTTCAGAAGGGTAGATGGAGTGTGGAGTGA	1158
Qy	222	oileLeuSerPheGlnThrPro-----ProSerAlaProLysAspValTrpValse	239
Db	1159	ATCATTGAGAACTCAAACTCCAGAGAAGAGCCCTACAGGGATGTACACGCTGGTACAT	1218
Qy	239	rGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeuTrpLys-----	256
Db	1219	GAACAGCACATTCAGCTACAAA---AGACAACAGATTATCTTCTGGGAAGAACTGTAG	1275
Qy	257	-----AlaProGlyProCysValGlnValSerTyzLysVal-----	268
Db	1276	TCTATCAGAGCGCAAGAAAATCTCTCCAC-----TATCAAGTGCCTTGCAGGAGGT	1329
Qy	269	-----TrpPheTrpValGI	273
Db	1330	CGCAGAGGGGAATGCCACATGCAGAAATATCATCTGAACGCAACTCTCTGGACCTGGACC--	1387
Qy	273	yGlyArgLeuLeuSerProGluGlyIleThrCysCysSerLeuIleProSerGlyAl	293
Db	1388	-----ATACCCAGAACTGG	1401
Qy	293	aGluTrp---AlaArgValSerAlaValAsnAla-----ThrSerTrpGluProLeuTh	310
Db	1402	CATCTGGCTGCGCGCGTGTGCGACTAATCTCCAAAGGCAGTTCCTCGCCACTCGTAT	1461
Qy	310	rAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValserSe	330
Db	1462	TAACATGAGACATGTGCGGAGCAGCGGTTGCTGGCTCTCTCAGCAGGTTTCTGCAAAACC	1521
Qy	330	rileAlaGlySerThrGluLeuLeuValThrTrp---GlnProGlyProGlyGluProLe	349
Db	1522	A---GAGGGCTCGGACAACTCTCTGGTGAAGTGGACGTCTCCGGGGGAAGGTGCCACTGC	1578
Qy	349	u-----GluHisValValAspTrpAlaArg-----AspGlyAspProLeuGluLy	364
Db	1579	TGTGCAGGAGTATGTGTGGAGTGGAGGGAGCTCCATCTCAGGGGTGGCATGCAGCCCC	1638
Qy	364	sLeuAsnTrpValArgLeuProProGlyAsnLeuSerAlaLeuLeuProGlyAsnPheTh	384
Db	1639	TCTAAGCTGCTGGGAGTCCCCCTACAACAGTCCACCTCATCTCAGACAAACATAAA	1698

Qy	384	rValGlyValProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAl	404
Db	1699	ACCTCATCTGTTATGAATTCGAGTCGACGCACTTTTCAGGGGAC--CAGGGAGGATG	1755
Qy	404	aSerSerValTIpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpAr	424
Db	1756	CAGTCTCATCCGGGGTGACTGAAGCATTAAGCACCACTGAGTGGCCCCCACATTAAATGC	1815
Qy	424	gLeuGlnAlaProProGlyThrProAlaIleAlaTIpGlyGluValProArgHisG1	444
Db	1816	CATCTCAGAG--GAAAGGGAGGACATTTTAATTTTCATGGGACGAAATTCAGCCCGAGG	1872
Qy	444	nLeuArgGlyHisLeuThrHisTyrThrLeuCys-----AlaGlnSerGlyThrSe	461
Db	1873	GCAAAATGGGCTGCATCTCTCATACAGGATCTATTGGAAGGACGGGATCCGATTCCTCA	1932
Qy	461	rProSerValCys-----MetAsnValSerGlyAsnThrGlnSerValThrLeuPr	478
Db	1933	GCCTCAGCTCTGTGAATTCCTTATAGAGTCTCCCCCAATCACATCCCATAGAGCCT	1992
Qy	478	oAspLeuProTIpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGlyGlnG1	498
Db	1993	GCAG--CCGAGAGTGACATACGTCTCTGTGGATGACAGCTCTGACAGCTGCTGGCGAAAG	2049
Qy	498	yProProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTIpLys----	516
Db	2050	CCCCAAGGAAATGACAGGGAATTTTGTCTG--CAGGTAAGCCCAATTTGAGGCACATT	2106
Qy	517	-ValLeuProGlyIle-----LeuPheLeuTIpGlyLeuPheLeuLeuGlyCysG1	533
Db	2107	TGTAGCACCAAGCATTTGCATTGCTGCTCATCAGTGGGCGTTTTC-----2152	
Qy	533	yLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArgHisLysValLeu-----	550
Db	2153	-----TCAATGCGTTGCTTCGGGCAAAAGGATTGTGTTCTCTCTTTGCG	2196
Qy	551	-----ProArgTIpValTIpGluLysValProAspProAlaAsnSerSerGlyG1	568
Db	2197	CCTCAGACCTCAGTGGTGTAGCAGAGAAATTCAGACCAGCCCAATAGACACTGGGCCAA	2256
Qy	568	nProHis-----MetGluGlnValProGluAlaGlnProLeuGlyAspLue	583
Db	2257	GAAATATCCCATTTGGAGGAGAGAAACAGCTGCTCCCTGGATAGGCTCTGGCAGACATG	2316
Qy	583	uProIleLeuGluValGluLwMetGluProProValMetGluSerSerGlnProAl	603
Db	2317	GCCCATCTCTGAA-----GAACCTGAGCCCTTGGTCATCAATGA-AGTCCTTC	2363
Qy	603	aGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeuProThrProGluG1	623
Db	2364	CTCAAGTGACTCCAGCTTTCAGAG-----CCCCCATCATCCCA	2402
Qy	623	uLeuGlyLeuLeuGlyProProArgProGln	633
Db	2403	ACTGGCCAGGAAAGGCAAAAGGCTCCCAAGG	2433

RESULT 13

US-10-641-643-1086  
 ; Sequence 1086, Application US/10641643  
 ; Publication No. US20040077003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; Susan G. Stuart  
 ; Jeffrey J. Sellhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE D  
 ; GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, I  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA

COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1086:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2943 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g183046  
SEQUENCE DESCRIPTION: SEQ ID NO: 1086 :  
US-10-641-643-1086

Alignment Scores:  
Pred. No.: 5,25e-17 Length: 2943  
Score: 297.50 Matches: 173  
Percent Similarity: 34.73% Conservative: 76  
Best Local Similarity: 24.13% Mismatches: 269  
Query Match: 8.50% Indels: 201  
DB: 17 Gaps: 33

US-10-088-950A-1 (1-636) x US-10-641-643-1086 (1-2943)

Qy 50 LeuAsnCysSerTrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGln 69  
Dy |||||  
Dy 587 CTCATCTGCCAGTGGGAGGACCTGAGACCCACCTACCCACAGCTTCACTCTGAG 646  
Qy 70 SerGlnLysTrpArgSerAsn---LysThrGlnThrValAlaVal----- 83  
Dy |||||  
Dy 647 AGTTTCAGAGCCGGGCACTGTGCAGACCCAGGGGACTCCATCTGGAGCTCGTGCCC 706  
Qy 84 AlaAlaGlyArgSerTrpValAlaAlaProArgGluGlnLeuThrMetSerAspLysLeu 103  
Dy |||||  
Dy 707 AAGGACGGGAGAGCCACTGTGTCATCCCGCAACACCTGTGTGTGTACCAAGATATG 766  
Qy 104 LeuValTrp-----GlyThrLysAlaGlyGlnProLeuTrp--- 115  
Dy |||||  
Dy 767 GGCATCTGGGTGGGAGGAGAGATGCGTGGGGACAGCATGTCCCAACACTGTGCTT 826  
Qy 116 -----ProProValPheValAsnLeuGluThrGlnMet 126  
Dy |||||  
Dy 827 GATCCCATGGATGTTGTGAACACTGGAGCCGCCCATGCTGCGACCATGGACCCAGCCCT 886  
Qy 127 LysProAsnAlaProArgLeuGly-----ProAspValAspPhe 139  
Dy |||||  
Dy 887 GAAGGGGCCCTCCCGCAGGAGGCTGCTACAGCTGTGCTGGAGCCA----- 934  
Qy 140 SerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHis 159  
Dy |||||  
Dy 935 -----TGGCAGCCAGGCTGCACATAAATCAG 961  
Qy 160 LysValLeuLeuCysGlnPhe---HisTyrArgArgCysGlnGluAlaAlaTrpThrLeu 178  
Dy |||||

Dy 962 AAG-----TGTGAGCTGCGCCCAAGCCGACGCTGGAGAGCCAGCTGGGCACTG 1012  
Qy 179 LeuGluProGluLeuLysThrLeuProLeuThrProValGluLeuGlnAspLeuGluLeu 198  
Dy |||||  
Dy 1013 GTGGGCCCC-----CTCCCTTGGAGGCCCTTCAGTATGAGCTC 1051  
Qy 199 -----AlaThrGlyTyrLysValTrpGlyArgCysArgMetGluLysGlu 213  
Dy |||||  
Dy 1052 TGGGGGCTCTCCAGCCACGGCTACACCTGCAGATACGCTGCATCCGCTGGCCCTG 1111  
Qy 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaPr 233  
Dy |||||  
Dy 1112 CTGGCCACTGGAGCGACTGGAGCCCGAGCTGAGCTGAGNACTACCGAACGGGCCCCC 1171  
Qy 233 oLysAspValTrpValSerGlyAsnLeuCysGly-----ThrProGlyGlyGluGluPr 251  
Dy |||||  
Dy 1172 ACTCTCAGACTGGACACATGTTGGCGCAGAGGAGCTGCAGCCCGAGGA-----CAGTG 1225  
Qy 251 oLeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTr 271  
Dy |||||  
Dy 1226 -CAGCTGTTCTGGAAG--CCAGTGCCTTGGAGAGACAGCGGAGCGATCCCAAGGTTA 1281  
Qy 271 pValGlyGlyArgGluLeuSerProGluGlyLleThrCysCysCysSerLeuLleProSe 291  
Dy |||||  
Dy 1282 TGTG-----GTTTCTTGGAGACCCCTC 1302  
Qy 291 rGlyValaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAs 311  
Dy |||||  
Dy 1303 AGCCAGGCTGGGCGCATCTGCCCTCTGCAACACCACAGAGCTAGCTGCACCTTCCA 1362  
Qy 311 nLeu-----SerLeuValCysLeuAspSerAla-----SerAl 322  
Dy |||||  
Dy 1363 CTGCTCTCAGAAGCCCGAGGAGTGGGCTTGTGGCTTATAACTCAGCCGGAGCTCTCG 1422  
Qy 322 aProArgSerValAlaValSerSerIleAlaGlySerThr----- 335  
Dy |||||  
Dy 1423 CCCACCCCGTGTGTTCTCAGAAAGCAGAGGCCAGCTCTGCAGAGCTCCATGCCAT 1482  
Qy 336 -----GluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuGln 350  
Dy |||||  
Dy 1483 GGCCCGAGACCCCTCACAGCTCTGGGTAGGTGGGAGCCCGCCCACTCATGCTCAGGG 1542  
Qy 350 uHisValValAspTrpAlaArgAspGlyAspProLeuGluLysLeuAsn---TrpVa 368  
Dy |||||  
Dy 1543 CTATGTGATTGATGGGCGCTGGGCGCCCGCCAGCGCAGCAATAGCAACAAGCTGGAG 1602  
Qy 368 lArgLeuProProGlyAsnLeuSerAla---LeuLeuProGlyAsnPheThrValGlyVa 387  
Dy |||||  
Dy 1603 GATGGAACAGAAATGGAGAGCCACGGGGTTCCTGCTGAAGGAGAACATCAGGCCCTTCA 1662  
Qy 387 lProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerVa 407  
Dy |||||  
Dy 1663 GCTCTATGATCATCGTGACTCTCCCTGTACAGGACACCATGGGAGCCCTCCAGCATGT 1722  
Qy 407 lTrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAs 427  
Dy |||||  
Dy 1723 CTATGCTACTCTCAAGAAATGGCTCCCTCCCATGCCCGCAGAGCTG---CATCTAAGCA 1779  
Qy 427 pAlaProProGlyThrProAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgL 447  
Dy |||||  
Dy 1780 CATTGGCAGACTGGGCACAGCTGGAGTGGGTGCTGAGCCCTCGAGCTGGGGAAGAG 1839  
Qy 447 yHisLeuThrHisTyrThrLeuCysAlaGlnSerGlyThrSerProSerValCysMetAs 467  
Dy |||||  
Dy 1840 CCCCCCTTACCCTACACCATCTTCTGGACCAACAGCTCAGAACCATCTCTTCGCGCAT 1899  
Qy 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487  
Dy |||||  
Dy 1900 CTGAATGCTCTCTCCCGTGGCTTGTCTCATGGCTGGAG-----CCGCGCAGCTCT 1953  
Qy 487 uTrp-----valTh 490  
Dy |||||  
Dy 1954 GTATCATCATCCACTCATGCTGCCAGCGCTGGGGCCACCAACAGTACAGTCTCTCAC 2013

QY 490 rAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgIleuHisLeuProAs 510  
| | | | | : : : : :  
Db 2014 CCGTATGACCTTGGACCCAGAGGGGTGC-----GAGCTACACATC----- 2053  
QY 510 pAsnThrLeuArgTrpLysValLeuProGlyLysLeuPheLeuTrpGlyLeuPheLeuLe 530  
| | | | | : : : : :  
Db 2054 -----ATCCTGGGCTGTGTGGGCTTCCTGCTGTT 2082  
QY 530 u-----GlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTrpHisLeuArgHi 547  
| | | | | : : : : :  
Db 2083 GCTCACCTGCCTCTGTGA-----ACTGCTGCTGCTGTGTGCAGCCCAACAG 2130  
QY 547 sLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerSeri 567  
| | | | | : : : : :  
Db 2131 GAAG-----AATCCCTCTGGCCAAAGTGTCCAGACCCAGCTCACAGCAGCTGGG 2181  
QY 567 y-----GlnProHisMetGluLysValPro-----GluAlaG1 578  
| | | | | : : : : :  
Db 2182 CTCTGGGTGCCCAATCATGGAGGAGATGCTTCCAGCTGCCGGCTTGCACGCC 2241  
QY 578 nProLeuGlyAspLeuProIleLeuGluValGluMetGluProPro----- 595  
| | | | | : : : : :  
Db 2242 ACCATCACCAGCTCACAGTGTGGAGGAGATGAAGAAGCGGTGCTGGGAGTC 2301  
QY 596 -----ValMetGluSe 599  
| | | | | : : : : :  
Db 2302 CCATAACAGCTCAGAGACCTGTGGCTCCCACTCTGGTCCAGACCTATGTCTCCAGGG 2361  
QY 599 rSerGlnProAlaGlnAlaThrPro---LeuAspSerGlyTrpGluLysHisPheLe 618  
| | | | | : : : : :  
Db 2362 GGACCCAAAGACGATTTCCACCCAGCCCAATCCAGTCTGGCACCAGCATCAGGTCCT 2421  
QY 618 u-----ProThrProGluLysLeuGlyPro----- 629  
| | | | | : : : : :  
Db 2422 TTATGGCAGCTGTGGGCAGCCCAACAGCCAGGCGCAGGCA-CTATCTCGCTGTG 2480  
QY 630 -----ProArgProGlnValLeu 635  
| | | | | : : : : :  
Db 2481 ACTCCACTCAGCCCTCTTGGCGGGCTCACCCGCCAGCCCAAGTCCTA 2529

## RESULT 14

US-10-252-157-457  
; Sequence 457, Application US/10252157  
; Publication No. US20030190640A1  
; GENERAL INFORMATION:  
; APPLICANT: Fatis, Mary  
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: PA-0027-1 US  
; CURRENT APPLICATION NUMBER: US/10/252,157  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 60/295,048  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 501  
; SOFTWARE: PERL Program  
; SEQ ID NO 457  
; LENGTH: 3139  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030190640A1 346686.23  
US-10-252-157-457

Alignment Scores:  
Pred. No.: 5.67e-17 Length: 3139  
Score: 297.50 Matches: 173  
Percent Similarity: 34.73% Conservative: 76  
Best Local Similarity: 24.13% Mismatches: 269  
Query Match: 8.50% Indels: 201  
DB: 16 Gaps: 33

US-10-088-950A-1 (1-636) x US-10-252-157-457 (1-3139)

QY 50 LeuAsnCysSerTrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGln 69  
| | | | | : : : : :  
Db 726 CTATCTGGCAGTGGGAGCCAGGACCTGAGACCCACCTACCCAGCCTTCACTCTGAAG 785  
QY 70 SerGlnLysTrpArgSerAsn---LysThrGlnThrValAlaVal----- 83  
| | | | | : : : : :  
Db 786 AGTTTCAAGACCGGGGCAACTGTCAAGACCAAGGGGACTCCATCTGGAGCTGGTGCCTC 845  
QY 84 AlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSerAspLysLeu 103  
| | | | | : : : : :  
Db 846 AAGACCGGCGAGACCCACTCTGCTATCCCAACCAACACCTGTGTGTACCAAAATATG 905  
QY 104 LeuValTrp-----GlyThrLysAlaGlyGlnProLeuTrp--- 115  
| | | | | : : : : :  
Db 906 GGCATCTGGTGGCAGGAGAGATGCGCTGGGACCAAGCATGCTCCCACTGTGTCTT 965  
QY 116 -----ProProValPheValAsnLeuGluThrGlnMet 126  
| | | | | : : : : :  
Db 966 GATCCCATGATGTTGTGAACCTGGAGCCCTCATGCTGGGACCATGGACCCCGACCT 1025  
QY 127 LysProAsnAlaProArgLeuGly-----ProAspValAspPhe 139  
| | | | | : : : : :  
Db 1026 GAAGCGGCCCTCCCGAGGAGGCTGCCTACAGCTGTGTGGGAGCCA----- 1073  
QY 140 SerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHis 159  
| | | | | : : : : :  
Db 1074 -----TGGCAGCAGCGCTGCACATAAATCAG 1100  
QY 160 LysValLeuLeuCysGlnPhe---HisTyrArgArgCysGlnGluAlaIleThrTrpLeu 178  
| | | | | : : : : :  
Db 1101 AAG-----TGTGAGCTGCCCAAGCCGCGTGGAGAGGACGCTGGGCACTG 1151  
QY 179 LeuGluProGluLeuLysThrIleProLeuThrProValGluLeuGlnAspLeuGluLeu 198  
| | | | | : : : : :  
Db 1152 GTGGGCCCT-----CTCCCTTGGAGGCCCTTCATATGAGCTC 1190  
QY 199 -----AlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213  
| | | | | : : : : :  
Db 1191 TGGGGGTCTCTCCAGCCAGCGCTACCCCTGAGATACCTGCTGCTGCTGCGCTGGCCCTG 1250  
QY 214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThr-ProProSerAlaPr 233  
| | | | | : : : : :  
Db 1251 CTTGGCCACTGGAGCAGCTGGAGCCCGCAGCTGGAGTGAAGTACCGAAGCGGCCCTC 1310  
QY 233 oLysAspValTrpValSerGlyAsnLeuCysGly-----ThrProGlyGlyGluGluPr 251  
| | | | | : : : : :  
Db 1311 ACTGTCAGACTGGACACATGTTGGCGGCAGAGGAGCTGGACCCAGGA-----CAGTG 1364  
QY 251 oLeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTr 271  
| | | | | : : : : :  
Db 1365 -CAGCTGTTCTGGAAG---CCAGTGCCCTGGAGGAAGACAGCGGAGGATCAAGGTTA 1420  
QY 271 pValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIleProSe 291  
| | | | | : : : : :  
Db 1421 TGTG-----GTTCTTGGAGACCTC 1441  
QY 291 rGlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAs 311  
| | | | | : : : : :  
Db 1442 AGCGAGGCTGGGGCCATCTCTGCCCTCTGCAACACACACAGAGCTCAGCTGCACCTTCCA 1501  
QY 311 nLeu-----SerLeuValCysLeuAspSerAla-----SerAl 322  
| | | | | : : : : :  
Db 1502 CTGCTTCCAGAACGCCAGAGGTGGCCCTTGTGGCTATACTACGCGGGGACCTCTCG 1561  
QY 322 aProArgSerValAlaValSerSerIleAlaGlySerThr----- 335  
| | | | | : : : : :  
Db 1562 CCCCACCCGGTGTCTTCTCAGAAAGACAGAGGCCCGCAGCTCTGACCCAGACTCCATGCCAT 1621  
QY 336 -----GluLeuLeuValThrTrpGlnProGlyProGlyGluProLeuG1 350  
| | | | | : : : : :  
Db 1622 GGCCCGAGACCTTCACAGGCTCTGGGTAGGTGGAGGCCGCCCAATCCATCCATGGCTCAGG 1681

QY 350 uHisValValAspTrpAlaArgAspGlyAspProLeuGluLysLeuAsn-----TrpVa 368  
Db 1682 CTATGTGATTGAGTGGGGCTGGGCCCCCCCCAGCGAGCAATAGCAACAAGACCTGGAG 1741  
QY 368 lArgLeuProProGlyAsnLeuSerAla---LeuLeuProGlyAsnPhetThrValGlyVa 387  
Db 1742 GATGGAACAAGATGGGAGAGCCACGGGGTTCTGCTGAAGAGGAACATCAGGCCCTTTCA 1801  
QY 387 lProTyraGileThrValThAlaValSerAlaSerGlyLeuAlaSerAlaSerSerVa 407  
Db 1802 GCTCTATGAGATCATGCTGACTCCCTGTACAGGACACCATGGGACCTCCACGATGT 1861  
QY 407 lTrpGlyPheArgGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAs 427  
Db 1862 CTTATGCTACTCTCAAGAAATGGCTCCCTCCATGCCAGAGCTG---CATCTAAGCA 1918  
QY 427 pAlaProProGlyThrProAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgGl 447  
Db 1919 CATTGCCAAGACTGGGCCACAGCTGGAGTGGGTGCTGAGCCCTCCAGCTGGGAAGAG 1978  
QY 447 yHisLeuThrHisTyThrLeuCysAlaGlnSerGlyThrSerProSerValCysMetAs 467  
Db 1979 CCCCCTTACCACATACACCATCTCTGGACCAAGCTCAGAACCATGCTCTCTCGCCAT 2038  
QY 467 nValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysGluLe 487  
Db 2039 CTTGAATGCTCTCCCGTGGCTTTGCTCTCCATGGCTGGAG-----CCGCGCAGTCT 2092  
QY 487 uTrp-----ValTh 490  
Db 2093 GTATCATCATCCACTGCTGCTCCAGCCAGGCTGGGGCCACCAACAGTACAGTCTCTAC 2152  
QY 490 rAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeuHisLeuProAs 510  
Db 2153 CTTGATGACCTTGACCCAGAGGGGTG-----GAGCTACACATC----- 2192  
QY 510 pAsnThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGlyLeuPheLeuLe 530  
Db 2193 -----ATCCTGGGCTGTCTGGGCTCTCTGCTGT 2221  
QY 530 u-----GlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArgHi 547  
Db 2222 GCTCACCCTGCTGTGGA-----ACTGCTGCTGTGTGAGCCCAACAG 2269  
QY 547 sLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerGly 567  
Db 2270 GAAG-----AATCCCTCTGGCCAGTGTCCAGACCCAGCTCAGACGACCTGGG 2320  
QY 567 Y-----GlnProHisMetGluGlnValPro-----GluAlaGl 578  
Db 2321 CTCTGGGTGCCCAATCATGTAGGAGAGATGCTTCCAGCTGCCGCGCTGGCAGGCC 2380  
QY 578 nProLeuGlyAspLeuProIleLeuGluValGluMetGluProPro----- 595  
Db 2381 ACCCATCACCAGCTCAGAGTCTGGAGGAGGATGAAGAGCGGTGCGCTGGGAGTC 2440  
QY 596 -----ValMetGluSe 599  
Db 2441 CCATAACAGCTCAGAGACCTGTGGCTCCCTCCACTCTGCTCCAGACCTATGTCTCCAGGG 2500  
QY 599 rSerGlnProAlaGlnAlaThrAlaPro---LeuAspSerGlyTyThrGluLysHisPheLe 618  
Db 2501 GGACCCAAAGACAGTTTCCACCCAGCCCAATCCAGTCTGGCACAGCGATCAGGTCTCT 2560  
QY 618 u-----ProThrProGluGluLeuGlyLeuLeuGlyPro----- 629  
Db 2561 TTATGGGCAGCTGCTGGGACGCCCAACAGCCAGGGCCAGGCA-CTATCTCGCTGTG 2619  
QY 630 -----ProArgProGlnValLeu 635  
Db 2620 ACTCCACTCAGCCCTCTTGGGGGCTCTCAGCCCGCCAGCCCAAGTCTCTA 2668

RESULT 15  
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; Sequence 134, Application US/103511157  
; Publication No. US20030215838A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Kuijper, Joseph L.  
; APPLICANT: Dasovich, Maria M.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Hammond, Angela K.  
; APPLICANT: No. US20030215838A1ak, Julia E.  
; APPLICANT: Gross, Jane A. R.  
; APPLICANT: Dillon, Stacey R.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
; FILE REFERENCE: 02-02  
; CURRENT APPLICATION NUMBER: US/10/351.157  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/435,361  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/389,108  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/350,325  
; PRIOR FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 134  
; LENGTH: 4026  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (780)...(3692)  
US-10-351-157-134  
  
Alignment Scores:  
Pred. No.: 5,06e-16 Length: 4026  
Score: 288.50 Matches: 157  
Percent Similarity: 35.45% Conservative: 89  
Best Local Similarity: 22.62% Mismatches: 275  
Query Match: 8.25% Indels: 173  
DB: 17 Gaps: 34  
1527 TTGGACTGTTCATGGGAACCT-----GGGGTAGATACGACTTTGACTTGGCGT 1574  
QY 50 LeuAsnCysSerTrpGluProLeuGlyAspLeuGlyAlaProSerGluLeuHisLeuGln 69  
Db 1527 TTGGACTGTTCATGGGAACCT-----GGGGTAGATACGACTTTGACTTGGCGT 1574  
QY 70 SerGlnLysTyArg-----SerAsnLysThrGlnThrVal 81  
Db 1575 AACCAAGATTCCAAACACTACACTTTATGTGAATCGTTCTCTAAGAGATGTGAGGTTCT 1634  
QY 82 AlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGln----- 96  
Db 1635 AACTCAGGAACCTCTCTATACCTGCGCAAAATCACTGAAGGCTCAGAGAAATGTATAACTTT 1694  
QY 97 ---LeuThrMetSerAspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrp 115  
Db 1695 ACTCTCAGAGCTGAAACCACTAAGGAAAGAAAGAGTGTCAAC----- 1736  
QY 116 ProProValPheValAsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyPro 135  
Db 1737 -----ATTAATTTAACTGACCCATAGTTCATCAAGGCTCCGAG----- 1781  
QY 136 AspValAspPheSerGluAspProLeuGluAlaThrValHisTrpAlaProProThr 155  
Db 1782 GAGCTCACCCTTAAATATTATAGGTGCTCAAAAGGCCAACATGACTTGGAGGTTCACTCC 1841  
QY 156 TrpProSerHisLysValLeuIleCysGlnPheHisTyArgArgCysGlnGluAlaAla 175



1842	Db	CATGGAAACAACATACACACACTTTTGTGTCAGGTTAAACTCCAATATGAGAA-----	1899
176	Qy	TrpThrLeuLeuGluProGluLeuLysThrIleProLeuThrProValGluIleGlnAsp	195
1893	Db	---GTGATTTCATGACGACCAATGTTCTGTCACATAGCGCAAACTACCTCTTCAGTGAT	1949
196	Qy	LeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGluGluAsp	215
1950	Db	CTGGATCCAGACACAAGATACAAAGCCTTTTGTGCGCTGTGCAAGTGCACACCACTTCTCGG	2009
216	Qy	LeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaProLys---	234
2010	Db	AAATGGAGCCTGGAGCCCAA---AAAGATTTCAGCACACCGAGACTGTCTCCTCCACAG	2066
235	Qy	----AspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeu	252
2067	Db	GCTCTTGATGATGG-----AGACAAGTGTGGTCGGAGAATGGAAGACCGCAATGTGACT	2120
253	Qy	LeuLeuTrpLysAlaProGlyProCysValGln-----ValSer	265
2121	Db	TTATTTCTGGAG-----CCACTATTAAATACAGGCCCAATGGCAAAATCATATCC	2171
266	Qy	TyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGluGlyIleThrCysCys	285
2172	Db	TATAATATA-----GTTGTAGAAATGAGCCCAACCACTGAGTCAGAACACTAC	2222
286	Qy	CysSerLeuIleProSerGlyAlaGluTrpAla-----	296
2223	Db	TGT-----GTCTGGCCACCAGCCCTCAGCACAAACCTGAGCCTT	2261
297	Qy	-----ArgValSerAlaValAsnAlaThrSerTrpGluProLeu	309
2262	Db	GACCTGCAACCTTACAAGATTGCGATCACAGCCAAACAACGATGGGGCATTCTCCT---	2318
310	Qy	ThrAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSer	329
2319	Db	GAGTCCTTGATGTCTCTTCTAATGATTTCTGGACACGAGGTCAAGAAAGAACAAATAAA	2378
330	Qy	SerIleAlaGlySerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluProLeu	349
2379	Db	GGTATAAAGATGCATTCAAT-----ATTCTTGGGAGCCGCTATCTGGACACGATG	2432
350	Qy	GluHisValValAspTrp-----AlaArgAspGlyAspProLeuGluLysLeuAsnTrpVal	368
2433	Db	GGCTATGTTGTGACTGTTGTGCATCTCCAGCACCAACGCTGTGATTTGTCAGTGGAG	2492
369	Qy	ArgLeuProProGlyAsnLeuSerAlaLeuLeuProGly---AsnPheThrValGlyVal	387
2493	Db	AACTTTGGTCCCAATACCACAGCCACCAATCACTCAGATGATTTTAAACACAGCGTC	2552
388	Qy	ProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSer---AlaSerSer	406
2553	Db	CGTTACAACCTTCAGAAATTTTGAAGGTCTGTGGAACAAAGCTGGTTAGTAGAGAA	2612
407	Qy	ValTrpGlyPheArgGluLeuAlaProLeuValGlyProThrLeuTrpArgLeuGln	426
2613	Db	CAAAAGAGGATACACCCAGGAACCTGGCTCTTTGGTGAATCCAAAGTG-----	2660
427	Qy	AspAlaProProGlyThrPro-----AlaIleAlaTrpGlyGluValProArgHis	443
2661	Db	GAGATTCTTACTCGACCCCTTAACCTCCTCGTTCTAAGATGGCCAGATTATGACGCGAC	2720
444	Qy	GlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAlaGlnSer-----	458
2721	Db	TTCAGGCTGGTTTTATAAAGGGTACCTCGTGTATGTGAATCCAAAGGAGATGCGAGTC	2780
459	Qy	-----GlyThrSerProSerValCysMetAsnVal	468
2781	Db	AACCAACCCCTGGGAAGGACCCCTCTCCAGATAATTCAGTCTCTGTAAATACGACATC	2840
469	Qy	SerGlyAsn---ThrGlnSerValThrLeuProAspLeu---ProTrpGlyProCysGlu	486
2841	Db	AATGGGTTCAGACACAAGACACTCACCGTGGAAAACTTCAGCCAGAGTCCCTCTATGAG	2900

Search completed: February 23, 2005, 09:15:24  
Job time : 997 secs

Qy	487	LeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProProGlyProIleLeuArgLeu	506
Db	2901	TTTTTCGTCACTCGTACACAGCGCTGGCCAGGACCAATGAACGTTTCACAAAGGTC	2960
Qy	507	HisLeuProAspEnThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpGly	526
Db	2961	ACAACTCCAGAT-----GCAGCGTCCCACATGCTGCTGCAGATCATCATCCCATGACC	3014
Qy	527	LeuPheLeuLeuGlyCysGlyLeuSerLeuAlaThrSerGlyArgCysTyrHisLeuArg	546
Db	3015	CTCTGCGCTTG-----CTCAGCATCATCTGC-----TCCTACTGG-----	3050
Qy	547	HisLysValLeuProArgTrpValTrpGluLys-----ValProAspProAla	562
Db	3051	-----AAAAGTCAGTGGGTGAAGAGAAGTGCTACCCCTGACATTTCCCAATCCGTAC	3101
Qy	563	AsnSerSer-----	565
Db	3102	AAGAGCAGCATTTGTCTACTATAAATCCAGAAGNATCCTCACTTAATGAATGTC	3161
Qy	565	-----	565
Db	3162	AAAGACTGCATTCCAGATGTCCTTGAAGTGATAAACAAGCAGACGCAAGACACAG	3221
Qy	566	-----SerGlyGlnProHisMetGluGlnValProGluAlaGlnProLeuGlyAsp	582
Db	3222	TGTTGAGGCTCTGGGAAACTTCATTTGAAGATGTACCCCAATGAAGCGCCAATC-----	3275
Qy	583	LeuProIleLeuGluValGluGluMetGluProProValMetGluSerSerGlnPro	602
Db	3276	GTGGCA---ACAGAAAGAGGATTCCTCAGGCGCCTGTGCCCTGCAATCTTCTTTGAGAATTTT	3332
Qy	603	AlaGlnAlaThrAlaProLeuAspSerGlyTyrGluLysHisPheLeu-----	618
Db	3333	ACTTACGATCAGTCAGCTTTTGTACTCTGGT-----TCCCATGGCCTCATTTCCAGGTCCC	3386
Qy	619	-----ProThrProGluGluLeuGlyLeuLeuGlyProPro	630
Db	3387	CTAAAGACACAGACACCAACTTTGACTATTTGGCTCCACCT	3428

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 04:25:18 ; Search time 5411 Seconds  
(without alignments)  
4474.011 Million cell updates/sec

Title: US-10-088-950A-1

Perfect score: 3498

Sequence: 1 MRGGGAPFWLPLPKALL.....FLPTPEELGLGPPRPQVLA 636

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Fgapop 6.0			7.0
Delop 6.0			Delext 7.0

Searched: 3423544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool/US10088950/runat\_18022005\_094500\_21835/app\_query.fasta\_1.775  
-DB=EST -QFMT=fascap -SUFFIX=rstc -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USR=US10088950 @CGN 1 1 3437 @runat\_18022005\_094500\_21835 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:	gb_est1.*
1:	gb_est1.*
2:	gb_est2.*
3:	gb_hic.*
4:	gb_est3.*
5:	gb_est4.*
6:	gb_est5.*
7:	gb_est6.*
8:	gb_gss1.*
9:	gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1734.5	49.6	2935	3 AK040457	Mus muscu
2	1376	39.3	900	4 BG756328	602713647
3	1281.5	36.6	783	7 CK000257	CK000257
4	1251	35.8	942	5 BQ957232	AGENCOURT
5	1225	35.0	896	4 BF984779	602308006
6	1201.5	34.3	911	5 BQ919454	AGENCOURT
7	1170.5	33.5	681	2 BF035293	601457184
8	1125	32.2	620	7 CV030371	9471 Full
9	1104	31.6	950	5 BQ927024	AGENCOURT

10	1082.5	30.9	1028	5	BM917928	BM917928
11	1065	30.4	731	4	BI905856	AGENCOURT
12	1057	30.2	942	4	BG332437	603062945
13	1017	29.1	821	7	CO880024	BOVGen.08
14	990	28.3	803	7	CF785854	AGENCOURT
15	961	27.5	570	2	AW575269	UI-HF-BKO
16	911	26.0	727	7	CN790247	4124813 B
17	878	25.1	497	5	EX283853	BX283853
18	864	24.7	579	5	BP337994	BP337994
19	863.5	24.7	1776	4	BG115874	602316865
C 20	862	24.6	660	5	EX919538	BX919538
C 21	862	24.6	660	5	EX919711	BX919711
22	851	24.3	713	7	CK834168	4058370 B
23	839	24.0	597	4	BM048281	603627680
24	838	24.0	447	7	CN287418	170006000
25	832	23.8	674	6	CB422972	596137 MA
26	807	23.1	467	2	BF827655	MR2-HN003
27	804	23.0	653	7	CN789181	4133608 B
28	790.5	22.6	567	4	B1847463	469302 MA
29	784.5	22.4	772	4	B1559169	603241254
30	781	22.3	495	4	BM762764	K-EST0043
31	781	22.3	710	4	BM761233	K-EST0041
32	781	22.3	711	4	BM760781	K-EST0041
C 33	778	22.2	484	2	BF826136	MR2-HN003
34	777	22.2	575	2	BE588616	194198 BA
35	775	22.2	541	4	BM843047	K-EST0120
36	764	21.8	504	4	BM842397	K-EST0119
37	754	21.6	452	4	BM761623	K-EST0042
38	739	21.1	895	4	BG419535	602448234
39	738	21.1	406	4	BM764289	K-EST0045
40	729	20.8	403	2	BF825319	MR2-HN003
41	725	20.7	403	2	BF825801	MR2-HN003
C 42	725	20.7	421	2	BF825871	MR2-HN003
C 43	724.5	20.7	421	2	BF828838	MR2-HN003
C 44	721	20.6	405	2	BF828608	MR2-HN003
45	717	20.5	403	2	BF829689	MR2-HN003

#### ALIGNMENTS

RESULT 1  
AK040457  
LOCUS  
DEFINITION  
AK040457 2935 bp mRNA linear HTC 03-APR-2004  
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched  
library, clone:A43009B21 product:T cell cytokine receptor, full  
insert sequence.  
AK040457 GI:26087864  
VERSION  
KEYWORDS  
SOURCE  
Meth. Enzymol. 303, 19-44 (1999)  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1  
Carninci, P. and Hayashizaki, Y.  
AUTHORS  
TITLE  
High-efficiency full-length cDNA cloning  
JOURNAL  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253  
PUBMED  
10349636  
REFERENCE  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
REFERENCE  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, F., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 PUBMED 11076861	QY	22	LeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGlnCys 41     
	Db	330	TTGACACGGTCTCTCGGCTCTCTCGGCGCCCTGACAGGAGTCCAGTCCAGTGC 389     
	QY	42	TyrGlyValGlyProLeuGlyAspLeuAanCysSerTrpGluProLeuGlyAspLeuGly 61     
	Db	390	TACAGCGTGGTCCCTGGGAATCCTGAACTGCTCTCTGGGAACCTTTGGCGGACCTGGAG 449     
	QY	62	AlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThrVal 81     
	Db	450	ACTCCACTGTGCTGATACACAGAGTCAGAAATAT----- 485     
	QY	82	AlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSerAsp 101     
	Db	485	----- 485     
	QY	102	LysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProVal-PheValAs 121     
	Db	486	-----GCACTCTGGCGCTCCCATTTTCAGATG-- 510     
	QY	121	nLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSerG 141     
	Db	511	-----AAGCAGACACACCCAGATCTTCTCAAGTGATATTTCTGA 554     
	QY	141	uAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLysVa 161     
	Db	555	GGAAGCAACCTCGAGGCCACTGTGCACTGGGGCCGCCCGTGTGGCCACCGCAGAAAGT 614     
	QY	161	LleuLleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGluPr 181     
	Db	615	TCTCATCTGTCTCGGTACAAAGGAATGCCAGCTGAAACATGGACCCCGCTGGAGGCC 674     
	QY	181	oGluLeuLysThrLleProLeuThrProValGluLleGlnAspLeuGluLeuAlaThrGl 201     
	Db	675	CGAGCTGAGACACATGGCTGATCTCTCTGAGATCAGAACCTGGACCTGGCACCTG 734     
	QY	201	YTrpLysValTyrGlyArgCysArgMetGluLysGluLysLeuTrpGlyGluTrpSe 221     
	Db	735	CTACCAGGTGTCTGGCGCTGCCAGTGGAGAACCGATATCCA---TGGGGCGAGTGGAG 791     
	QY	221	rProLleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGlyAs 241     
	Db	792	TTGGCCCTGTCTCTTCAGACGCCATCTTATAGATCTCTGAGATGTGTGGGTATCGGGAC 851     
	QY	241	nLeuCysGlyThrProGlyGlyGluGluProLeuLeuLeuTrpLysAlaProGlyProCy 261     
	Db	852	CGTCTGTGAACTTCTGGCAACGGGACGCCCTGTCTGTCTGGAAGGAGCCCAAGACCTTG 911     
	QY	261	sValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGluGl 281     
	Db	912	TGTGACAGGTGACTTACAGTCTGGTTTGGGGCTGGAGATATTACTACACTCAAGAAGA 971     
	QY	281	vtileThrCysCysCysSerLeuLleProSerGlyAlaGluTrpAlaArgValSerAlaVa 301     
	Db	972	GGTCCCGTGTGCAAGTCCCTGTCTGATGGATGGAGTGGGTGTGTCTCTCTCTGG 1031     
	QY	301	IAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSerAlaSe 321     
	Db	1032	CAACAGCACAGTGGGTGGTCTCCACCAACCTGTCTCTCTCTC-----CAGAA-TC 1081     
	QY	321	rAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThrTr 341     
	Db	1082	TGCCCCCTGTGACGTGGGAGTGAGGAGTGGTGGAGCCCGGAGTAAGGTGACCTG 1141     
	QY	341	pGlnProGlyProGlyGluProLeuGluHisValValAspTrpAlaArgAspGlyAspPr 361     
	Db	1142	GAAACAGGACACGAGAAACCGTTGGAGTATGTGGTGGAGTGGGTCAAGATGGTGACAG 1201     
	QY	361	oLeuGluLysLeuAsnTrpValArgLeuProGlyAsnLeuSerAlaLeuLeuPro-- 380     
	Db	1202	CCTGGACAAAGCTCAACTGGACCCGCTCTCCCTCCCTGGAAACCTCAGACATTTGTACAGG 1261     
	QY	380	----- 380     

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2935) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/	QY	221	rProLleLeuSerPheGlnThrProProSerAlaProLysAspValTrpValSerGlyAs 241     
FEATURES	Location/Qualifiers	QY	261	sValGlnValSerTyrLysValTrpPheTrpValGlyGlyArgGluLeuSerProGluGl 281     
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ORIGIN	US-10-088-950A-1 (1-636) x AK040457 (1-2935)	QY	321	rAlaProArgSerValAlaValSerSerIleAlaGlySerThrGluLeuLeuValThrTr 341     

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 Qy 400 lyLeuAlaSerValTrpGlyPheArgGluLeuAlaProLeuValGlyP 420  
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 Qy 420 roThrLeuTrpArgLeuAlaProProGlyThrProAlaIleAlaTrpGlyGluV 440  
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 mRNA sequence.  
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US-10-088-950A-1 (1-636) x BG756328 (1-900)  
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 Qy 300 AlaValAsnAlaThrSerTrpGluProLeuThrAsnLeuSerLeuValCysLeuAspSer 319  
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 Qy 380 ProGlyAsnPheThrValGlyValProTyrArgIleThrValThrAlaValSerAlaSer 399  
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Alignment Scores:  
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 Query Match: 39.34% Indels: 9  
 DB: 4 Gaps: 0

ORIGIN  
 Note: this is a NIH\_MGC Library.  
 Site 2: EcoRI, cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Size-selected  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library.

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 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Size-selected  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

REFERENCE  
 1 (bases 1 to 900)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1CM1700 row: n column: 12  
 High quality sequence stop: 750.

ORGANISM  
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 (bases 1 to 900)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1CM1700 row: n column: 12  
 High quality sequence stop: 750.

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 400 GlyLeuAlaSerAlaSerValTrpGlyPheArgGluLeuAlaProLeuValGly 419  
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 422 CCAACGCTTTGGGAGTCCAAAGATGCCCTCCAGGACC-CCGCCATAGCGTGGGAGAG 480  
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CK000257 783 bp mRNA linear EST 26-NOV-2003  
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 CK000257.1 GI:38526291  
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 NIH-MGC <http://mgs.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [gsaps-r@mail.nih.gov](mailto:gsaps-r@mail.nih.gov)  
 Tissue Procurement: James Martin, University of Iowa  
 cDNA Library Preparation: M. Bento Soares, University of Iowa  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: Agencourt Bioscience Corporation  
 found through the I.M.A.G.E. Consortium/LNL at:  
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 Site 2: NotI; Library is oligo-dT primed and directionally  
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 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to RNA size fraction, ligated with  
 EcoR I adaptor, digested with Not I and then cloned  
 directionally into pYX-Asc vector. Average insert size  
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 (TATACGACTCACTATAGG)3'. Library was constructed in the  
 laboratory of M. Bento Soares. Average insert size 3-4kb  
 Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
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 Best Local Similarity: 96.81% Mismatches: 7  
 Query Match: 36.64% Indels: 3  
 DB: 7 Gaps: 1

US-10-088-950A-1 (1-636) x CK000257 (1-783)

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 QY 394 ThrAlaValSerAlaSerGlyLeuAlaSerAlaSerValTrpGlyPheArgGluGlu 413  
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Qy 414 LeuAlaProLeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrPro 433  
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 VERSION BQ957232.1 GI:22372710  
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 Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: DCTD/PTP  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN  
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US-10-088-950A-1 (1-636) x BQ957232 (1-942)

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Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40  
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Qy 239 rGlyAsnLeuCysGlyThrPro-GlyGlyGluProLeu-LeuLeu-TrpLysAlaPr 258  
 Db 849 GGAACCTCTGGGGGGAAGCCCTGAAAGAAAGAACCTTTGGCTTCTTAATGGAAGGCC 908

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 VERSION BQ984779.1 GI:12387591  
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 Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Inyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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Location/Qualifiers  
1. .896

#### FEATURES

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/db\_xref="taxon:9606"  
/clone="IMAGE:439248"  
/tissue\_type="duodenal adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 88"  
/note="Organ: small intestine; Vector: pCMV-SPORT6;  
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;  
oligo-dt primed. Average insert size 1.767 kb. Library  
enriched for full-length clones and constructed by Life  
Technologies. Note: this is a NIH\_MGC Library."

#### ORIGIN

Alignment Scores:  
Pred. No.: 4.3e-85 Length: 896  
Score: 1225.00 Matches: 248  
Percent Similarity: 83.77% Conservative: 5  
Best Local Similarity: 82.12% Mismatches: 27  
Query Match: 35.02% Indels: 25  
DB: 4 Gaps: 6

US-10-088-950A-1 (1-636) x BF984779 (1-896)

154 ProThrpAlaArgValSerHisLysValLeuLeuValCysGlnPheHisTyrArgArgCysGlnGlu 173  
2 CCTACATGGCCATCTCATAAAGTTCTGATCGCAGTTCCTACCTACCGAAGATGTCAGGAG 61  
174 AlaAlaTrpThrLeuLeuGluProGluLeuValThrIleProLeuThrProValGluIle 193  
62 GCGGCTGGACCTGCTGGAAACCGAGCTGAAGACCATACCTCCCTGACCTGTTGATC 121  
194 GluAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLysGlu 213  
122 CAGATTGGAGCTAGCCATGCTGCTACAAAGTGTATGCGCGCTGCGGATGAGAAAGAA 181  
214 GluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrProProSerAlaPro 233  
182 GAGGATTGTGGGCGAGTGGAGCCCAT-TTGTCTCTCCAGACACCGCTTCTGTCTCA 240  
234 LysAspValTrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGluProLeuLeu 253  
241 AAGATGTGTGGGATCAGGAAACCTCTGTGGACGCTCGAGAGAGGAGACCTTTGCTT 300  
254 LeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTrpPheTrpValGly 273  
301 CTATGGAAGCCCGAGGCGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360  
274 GlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIleProSerGlyAla 293  
361 GGTGCTGAGTGTGAGTGTGAGGAGGAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
294 GluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGluProLeuThrAsnLeuSer 313  
421 GAGTGGGCGCAGTG-TCCGCTGTCAAGCCACAGCTGGGAGCTCTCACCACTCTCT 479  
314 LeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSerSerIleAlaGly 333  
480 TTGTCTCTTTGGATTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539  
334 SerThrGluLeuLeuValThrTrpGlnProGlyGluProLeuGluHisValVal 353  
540 AGCAGGAGCTACTGTGTGACCTGGCAACCGGGGCTGCGGAGAACCTCTGGAGCATGTAGTG 599

354 AspTrpAlaArgAspGlyAspProLeuGluLysLeuAsnTrpValArgLeuProGly 373  
600 GATGGGCTCGATGGGACCCCTG-GAGAACTCACTGGGTCCGGCTTCCCTCGG 658  
374 AsnLeuSerAlaLeu---LeuProGlyAsnPheThrValGlyValProTyrArgIleThr 392  
659 AAACCTGAGTGTCTGTGTACACAGCGCATTTTCACTGTCCGGGTCCTATCGAATCACT 718  
393 ValThrAlaValSerAlaSerGly-----LeuAlaSerAlaSer----- 406  
719 GTGAACCGGAGCTCTGCTTCAGCTTGGCCCTCATCTCCGCTGGGGGTCTACGGGGTT 778  
407 -----ValTrpGlyPheArgGluGluLeuAlaProLeuValGly 419  
779 TTCCCCCTGTGTGGGCACACCTTTGGGATTGAGA-----ATGGCTCTGGAGACCCG 832  
420 ProThrLeuTrpArgLeuGlnAspAlaProProGlyThr-----ProAlaIleAla 436  
833 CCTATGTGTGG-----GGACGCGCTCCGGGAGTTTGGCGCTCCCCACATCGTG 883  
437 TrpGly 438  
884 TGGGG 889

RESULT 6  
BO919454 911 bp mRNA linear EST 20-AUG-2002  
LOCUS AGENCOURT 8822053 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6381506  
DEFINITION 5', mRNA sequence.  
ACCESSION BO919454  
VERSION BO919454.1 GI:22334152  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/BTP

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLMW2571 row: n column: 03  
High quality sequence stop: 619.

Location/Qualifiers  
1. .911

#### FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6381506"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

#### ORIGIN

Alignment Scores:  
Pred. No.: 3.01e-83 Length: 911  
Score: 1201.50 Matches: 245

Percent Similarity: 90.51% Conservative: 3  
 Best Local Similarity: 89.42% Mismatches: 10  
 Query Match: 34.35% Indels: 17  
 DB: 5 Gaps: 3

US-10-088-950A-1 (1-636) x BQ191454 (1-911)

QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20  
 Db 107 ATGGGGGAGGAGGAGGCGCCCTTCTGGCTGTGGCGCTGCCCAAGCTGGCGCTGCTG 166

QY 21 ProLeuLeuTrpValLeuPheGlnArgPrgProGlnGlySerAlaGlyProLeuGln 40  
 Db 167 CCTCTGTGTGGGTGCTTTTCAGCGGACGCTGCCAGGCGCGCGCGGCCACTGCAG 226

QY 41 CysTyrGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60  
 Db 227 TGCTACGGAGTTGGACCCCTGGCGGACTTGACCTGCTGTGGAGGCTCTTGGGGAGCTG 286

QY 61 GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80  
 Db 287 GGAGCCCTCCGAGTTACACCTCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT 346

QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaIleProArgGluGlnLeuThrMetSer 100  
 Db 347 GTGGCAGTGGCAGCGGACGAGCTGGGTGGCCATTCTCGGGAAACAGCTCACCATGTCT 406

QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProValPheVal 120  
 Db 407 GACAACTCTTGTCTGGGACACTAAGCAGCGCCAGCTCTCTGCGCCCGCTTCTGCTG 466

QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140  
 Db 467 AACCTAGAAACCCAAATGAACCAACAGCCCGCGCTGGGCCCTGACGTGGACTTTTCC 526

QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProTrpProSerHisLys 160  
 Db 527 GAGGATACCCCTGGAGGCGCACTGTCCATTGGGCCCCACCTACATGGCCACTTCATANA 586

QY 161 ValLeuIleCysGlnPheHisTyrArgArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180  
 Db 587 GTTCTGATCTGCCAGTTCACCTACCGAAGATGTCCAGAGGCGGCTGGACCTGCTGGAA 646

QY 181 ProGluLeuLysThrIleProLeu-ThrProValGluIleGlnAspLeuGluLeuAlaThr 200  
 Db 647 CCGAGCTGAAGACCAATACCCCTGGACCCCTGTGTGAGATCCAAGATTTGGAGCTAGCCAC 706

QY 200 rGlyTyrLysValTyrGly--ArgCysArgMetGluLysGluGluAspLeuTrp-GlyG1 219  
 Db 707 TGGCTACAAAGTGTATGGGNCCTGTCGGATGGAGAAAGAAAGGATTTGTGGGGCGA 766

QY 219 uTrp-SerProIleLeuSer-PheGlnThrPro-ProSerAla-ProLysAspVal-Trp 237  
 Db 767 GTGGAACCCCAATTTGTCCCTTCCAGACCGGCTTCTGTCTTCCAAAGATGTGTGG 826

QY 238 Val---SerGlyAsn---LeuCysGlyThrProGlyGlyGluGlu----- 250  
 Db 827 GTTATCCAGGAAACNTCTGTGTGGGAACCCCTT-GGGGAGAAAGGAAACCTTTT 885

QY 251 ProLeuLeuLeuTrpLysAlaPro 258  
 Db 886 GCCTTTCTAATGGGAAAGGGGCC 909

RESULT 7  
 LOCUS BF035293  
 DEFINITION 601457184F1 NIH\_MGC\_66 Homo sapiens cdna clone IMAGE:3860781'5', mRNA sequence.  
 ACCESSION BF035293  
 VERSION BF035293.1 GI:10743020  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 681)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: L1AM9596 row: g column: 22  
 High quality sequence start: 25  
 High quality sequence stop: 678.

## FEATURES

source 1..681  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3860781"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_66"  
 /notes="Organ: ovary; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,02e-81 Length: 681  
 Score: 1170.50 Matches: 215  
 Percent Similarity: 95.15% Conservative: 1  
 Best Local Similarity: 94.71% Mismatches: 9  
 Query Match: 33.46% Indels: 2  
 DB: 2 Gaps: 1

US-10-088-950A-1 (1-636) x BF035293 (1-681)

QY 131 ProArgLeuGlyPro---AspValAspPheSerGluAspAspProLeuGluAlaThrVal 149  
 Db 1 CCGCGTCTGGGTCCCTGACTGTGGACTTTTCGAGGATGACCCCTGGAGGCCACATGTC 60

QY 150 HisTrpAlaProProThrTrpProSerHisLysValLeuIleCysGlnPheHisTyr-Ar 169  
 Db 61 CATTTGGGCCCCACCTACATGGCCATCTCATAAAGTTCTGATCTGCCAGTTCCACTATCCG 120

QY 169 gATgCysGlnGluAlaAlaTrpThrLeuLeuGluProGluLeuLysThrIleProLeuTh 189  
 Db 121 AAGATGTCTCAGGAGCGCGGCTGGACCTCTGTGGAAACCGGAGCTGAAGACCATACCCCTGAC 180

QY 189 rProValGluIleGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCysAr 209  
 Db 181 CCTGTCTGAGATCCAGATTGGAGTAGCCACTGCTACAAAGTGTATNGCCGCTGCCG 240

QY 209 gMetGluLysGluGluAspLeuTrpGlyGluTrpSerProIleLeuSerPheGlnThrPr 229  
 Db 241 GATGGAGAAAGAGAGGATTTGTGGGCGGAGTGGAGCCCATTTAGTCTTCCAGACACC 300

QY 229 oProSerAlaProLysAspValTrpValSerGlyAsnLeuLysGlyThrProGlyGlyG1 249  
 Db 301 GCCTTCTGTCTCCAAAAGATGTGGGTATCAGGGAACCTCTGTGGAGCGCTGGAGAGA 360

QY 249 uGluProLeuLeuLeuTrpLysAlaProGlyProCysValGlnValSerTyrLysValTr 269  
 Db 361 GGAACCTTGTCTTATGAAGGCCCCAGGCGCTGTGTGAGGTGAGCTACAAAGTCTG 420

QY 269 pPheTrpValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysSerLeuIle 289

Db 421 GTTCTGGGTTGAGGTCGTGAGCTGAGTCCAGAGGAATTACCTGCTGCTCCTAAT 480

QY 289 eProSerGlyAlaGluTrpAlaArgValSerAlaValAlaThrSerTrpGluProLe 309

Db 481 TCCAGTGGGGGAGTGGCCAGGCTGTCCGCTGTCAACGCCACAAAGTGGAGCTCT 540

QY 309 uThrAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaValSe 329

Db 541 CAGCAAGCTCTCTTAGGTCGTGTTGATTCAGCCCTTGCCGCCGTAGCTGGCAGT 600

QY 329 rSerIleAlaGlySerThrGluLeuValThrTrpGlnProGlyProGlyGluProLe 349

Db 601 CAGCATCGTGGGACGACGACTACTGTGACCTGGCAACCGGGCCCTGGGGACCACT 660

QY 349 uGluHisValValAspTrp 355

Db 661 CGAGCATGTAGTGGACTGG 679

RESULT 8

CV030371 620 bp mRNA linear EST 20-AUG-2004

LOCUS 9471 Full length cDNA from the Mammalian Gene Collection Homo

DEFINITION sapiens cDNA 5' similar to BC028003, mRNA sequence.

ACCESSION CV030371

VERSION CV030371.1 GI:51488621

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 620)

Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,

Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,

Clingingsmith,T.R., Hartley,J.L., Esposito,D., Chao,D., Moore,T.,

Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,

Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.

Human ORFeome Version 1.1: a Platform for Reverse Proteomics

Genome Res. (2004) In press

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence tag (OST) of Gateway Entry construct. Each cloned ORF

results from a PCR reaction using an MGC full-length cDNA as

template DNA and ORF specific primers

PCR Primers

FORWARD: ATCGGGGAGGCGGGGCGC

BACKWARD: CAGGCCAGAACCTGTGGC

Insert Length: 620 Std Error: 43.00

Plate: 11070 row: 06 column: H

Seq primer: ACTGGCGTCGTGTTTACAACGTCGTGACTGGGAAC

High quality sequence start: 99

High quality sequence stop: 619

FOLTA=NO. Location/Qualifiers

1. 620

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="mixed"

/clone\_lib="Full Length cDNA from the Mammalian Gene

Collection"

/notes="Vector: mixed; The ORFs were PCR amplified from the

MGC (Mammalian Gene Collection) as of April 2004 and

cloned by recombinational Gateway cloning into pDONR223

Donor vector. Reference : MGC (Mammalian Gene Collection)

Program Team, Generation and Initial Analysis of more than

15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,

2002, 99(26), 16899-16903"

ORIGIN

# Alignment Scores:

Pred. No.: 1.54e-77 Length: 620

Score: 1125.00 Matches: 204

Percent Similarity: 99.51% Conservative: 1

Best Local Similarity: 99.03% Mismatches: 1

Query Match: 32.16% Indels: 0

DB: 7 Gaps: 0

US-10-088-950A-1 (1-636) x CV030371 (1-620)

QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20

Db 1 ATCGGGGAGGACAGGGGGCCCTTTCTGGCTGTGGCGCTGCCAAGCTGGCGCTGCTG 60

QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

Db 61 CCTCTGTGTGGTGTCTTTTCCAGCGACGCGTCCCGAGGCGCGCGGCGGCGCACTGCG 120

QY 41 CysTrpGlyValGlyProLeuGlyAspLeuAsnCysSerTrpGluProLeuGlyAspLeu 60

Db 121 TGCTACGGAGTTGGACCTTTGGGGGACTTGAACCTGCTCGTGGGAGCTCTTTGGGACCTG 180

QY 61 GlyAlaProSerGlyLeuHisLeuGlnSerGlnLysTrpArgSerAsnLysThrGlnThr 80

Db 181 GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAGTACCGTTCCAAACAAACCCAGACT 240

QY 81 ValAlaValAlaAlaGlyArgSerTrpValAlaLeuProArgGluGlnLeuThrMetSer 100

Db 241 GTGGCAGTGGCGCGGACGAGCTGGTGGCCATTCCTCGGGAACAGCTCACCATGTCT 300

QY 101 AspLysLeuLeuValTrpGlyThrLysAlaGlyGlnProLeuTrpProProValPheVal 120

Db 301 GACAAACTCTTGTCTGGGGACCTAAGCAGCAGCCAGCTCTCTGGCCCCCGCTCTTCGTG 360

QY 121 AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140

Db 361 AACCTAGAAACCCAAATGAAGCCAAAACGCCCCCGGCTGGGCGCTGAGCTGACTTTTCC 420

QY 141 GluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSerHisLys 160

Db 421 GAGGATGACCCCTGGAGGCGCAGCTGTCCATTGGGCCCCACCTAGATGCCATCTCATAAA 480

QY 161 ValLeuIleCysGlnPheHisTrpArgCysGlnGluAlaAlaTrpThrLeuLeuGlu 180

Db 481 GTTCTGATCTGCCAGTTCCATACCGAAGATGTCAAGAGGGGGCTGGACCTGCTGGAA 540

QY 181 ProGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAlaThr 200

Db 541 CGGAGAGCTGAAGACCATACCCCTGACCCCTGTGAGATCCAAAGATTGGAGCTAGCCACT 600

QY 201 GlyTrpLysValTrpGly 206

Db 601 GGCTANCAAGTGTATGGC 618

RESULT 9

BQ927024 950 bp mRNA linear EST 20-AUG-2002

LOCUS AGENCOURT\_8779973 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6382739

DEFINITION 5', mRNA sequence.

ACCESSION BQ927024

VERSION BQ927024.1 GI:22342055

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 950)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

## FEATURES

source

```

Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2575 row: a column: 12
High quality sequence stop: 469.
Location/Qualifiers
1..950
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6382739"
/tissue_type="carcinoma, cell line"
/lab_host="DHI0B (phage-resistant)"
/clone_lib="NIH MGC 40"
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

```

## ORIGIN

Alignment Scores:	
Pred. No.:	1.31e-75
Score:	1104.00
Percent Similarity:	85.42%
Best Local Similarity:	81.60%
Query Match:	31.56%
DB:	5
	Gaps: 3
	Indels: 15
	Mismatches: 28
	Conservative: 11
	Matches: 235
	Length: 950

US-10-088-950A-1 (1-636) x B0927024 (1-950)

Qy	1	Met	Arg	Gly	Gly	Arg	Gly	Ala	Pro	Phe	Trp	Leu	Trp	Pro	Leu	Pro	Lys	Leu	Ala	Leu	Leu	20
Db	107	AT	G	G	G	G	G	A	C	G	G	G	C	C	T	T	T	C	T	G	G	166
Qy	21	Pro	Leu	Leu	Trp	Val	Leu	Phe	Gln	Arg	Thr	Arg	Pro	Gln	Gly	Ser	Ala	Gly	Pro	Leu	Gln	40
Db	167	C	C	T	C	T	G	T	G	T	G	G	G	T	T	T	C	C	A	C	G	226
Qy	41	Cys	Tyr	Gly	Val	Gly	Pro	Leu	Gly	Asp	Leu	Asn	Cys	Ser	Trp	Glu	Pro	Leu	Gly	Asp	Leu	60
Db	227	T	G	T	A	C	G	G	A	G	T	T	C	C	C	C	A	G	G	C	G	286
Qy	61	Gly	Ala	Pro	Ser	Glu	Leu	His	Leu	Gln	Ser	Gln	Lys	Tyr	Arg	Ser	Asn	Lys	Thr	Gln	Thr	80
Db	287	G	G	A	C	C	C	C	C	T	C	C	A	G	C	C	A	A	A	A	A	346
Qy	81	Val	Ala	Val	Ala	Ala	Gly	Arg	Ser	Trp	Val	Ala	Leu	Pro	Arg	Glu	Gln	Leu	Thr	Met	Ser	100
Db	347	G	T	G	C	A	G	T	G	G	C	A	G	C	G	A	G	T	G	C	C	406
Qy	101	Asp	Lys	Leu	Leu	Val	Trp	Gly	Thr	Lys	Ala	Gly	Gln	Pro	Leu	Trp	Pro	Pro	Val	Phe	Val	120
Db	407	G	A	C	A	A	A	C	T	C	T	G	T	G	G	G	C	A	T	C	T	466
Qy	120	I	Asn	Leu	Glu	Thr	Gln	Met	Lys	Pro	Asn	Ala	Pro	Arg	Leu	Gly	Pro	Asp	Val	Asp	Phe	140
Db	467	G	A	A	C	T	A	G	A	A	C	C	A	A	G	C	C	C	C	C	C	526
Qy	140	er	Glu	Asp	Asp	Pro	Leu	Glu	Ala	Thr	Val	His	Trp	Ala	Pro	Pro	Thr	Trp	Pro	Ser	His	159
Db	527	C	C	G	A	G	G	A	T	A	C	C	C	C	T	G	C	A	T	T	G	586
Qy	160	Lys	Val	Leu	Leu	Cys	Gln	Phe	His	Tyr	Arg	Arg	Cys	Gln	Glu	Ala	Ala	Leu	Thr	Thr	Leu	179
Db	587	A	A	A	G	G	T	C	T	G	C	A	G	T	T	C	A	T	C	A	C	646

Qy	180	GluproGluLeuLysThrIleProLeuThrProValGluIleGlnAspLeuGluLeuAla	199
		:::	
Db	647	GAACCGACCTGAAGACCATACCCCTGACCCCTGTTGAGAT-CAAGATTTGGAGCTAGCC	705
Qy	200	ThrGlyTyrLysValTyrGlyArgCys-ArgMetGlu-LysGluGluAsp-LeuTyr-Gl	218
		:::	
Db	706	ACTGGCTACCAACGGGATGCGCGTCCCGATGGACAAACAACATGATTTTCTGGGGG	765
Qy	218	yGluTyrSerProIleLeuSer---PheGlnThrPro-ProSerAlaProLysAsp-val	236
		:::	
Db	766	CAAATGAACACCCCAATTTTGGCCCTTTCCAGACACCGCCCTTCGTCCAAAAAATGGGG	825
Qy	237	TrpValSerGlyAsnLeuCysGlyThrProGlyGlyGluGlu-----ProLeuLeuLeu	254
		:::	
Db	826	GGGGTATCCGGGAAACCCCGCGGTGGCCCTCGGAAGGAAAGAAACCCCTTTGTTTCTA	885
Qy	255	Trp-LysAlaPro---GlyProCysValGlnValSerTyrLysValTrpPheTrpValGl	273
		:::	
Db	886	TGGGAAGGCCCCCAGGGGCCCCCTGTGCGGAAGTTGAACCTCACCAAAAGCTGGGGTCTTTGG	945
Qy	273	yGly	274
Db	946	GGGG	949

## RESULT 10

BM9117928	1028 bp	linear	EST 12-MAR-2002
LOCUS			
DEFINITION	AGENCOURT 6614532 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5485274		
	5', mRNA sequence.		
ACCESSION	BM9117928		
VERSION	BM9117928.1 GI:19368307		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1028)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		

## REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-i@mail.nih.gov](mailto:cgapbs-i@mail.nih.gov)  
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

## FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:5485274"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 106"
/notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC library."

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## ORIGIN

Alignment Scores:  
Pred. No.: 7.05e-74 Length: 1028

Score: 1082.50 Matches: 240  
Percent Similarity: 65.39% Conservative: 17  
Best Local Similarity: 61.07% Mismatches: 62  
Query Match: 30.95% Indels: 75  
DB: 5 Gaps: 11

US-10-088-950A-1 (1-636) x BM917928 (1-1028)

QY 248 GlyGluGluProLeuLeuLeuTrpValAlaProGlyProCysValGlnValSerTyrIlys 267  
DB 3 GGAGAGAAACCTTGTCTTATGGAAGGCCCGAGGCCCTGTGTGAGTAGAGTACAA 62  
QY 268 ValTrpPheTrpValGlyArgGluLeuSerProGluGlyIleThrCysCysSer 287  
DB 63 GTCTGCTTCTGGGTGGAGTGTGAGCTGAGTGCAGAGGAATTACCTGTCTGCTCC 122  
QY 288 LeuIleProSerGlyAlaGluTrpAlaArgValSerAlaValAsnAlaThrSerTrpGlu 307  
DB 123 CTAATTCCAGTGGGGCGAGTGGCGAGGTGTCCGTGTCAAGGCCCAAGCTGGGAG 182  
QY 308 ProLeuThrAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAla 327  
DB 183 CCTCTCACCACCTCTCTTGTGCTCTTGGATTCAGCCTCTGCCCTCTGAGCTGGGA 242  
QY 328 ValSerSerIleAlaGlySerThrGluLeuLeuValThrTrpGlnProGlyProGlyGlu 347  
DB 243 GTCAGCAGCATCGCTGGGAGCAGGAGCTACTGGTGACCTGGCAACCGGGCTGGGAA 302  
QY 348 ProLeuGluHisValValAspTrpAlaArgAspGlyAspProLeuGluIlysLeuAsnTrp 367  
DB 303 CCACCTGGAGCATGTAGTGGACTGGCTCGAGATGGGACCCCTGTGGAGAACTCAACTGG 362  
QY 368 ValArgLeuProGlyGluLeuSerAlaLeuLeuProGlyAsnPheThrValGlyVal 387  
DB 363 GTCGGGCTTCCCTCGGACCTCAGTCTCTGTACAGGGAATTTACTGTGGGGTTC 422  
QY 388 ProTyrArgIleThrValThrAlaValSerAlaSerGlyLeuAlaSerAlaSerVal 407  
DB 423 CCTATCGAATCATCTGACCGCACCTCTGCTTTCAGGCTGGGCTCTGCATCTCCGTC 482  
QY 408 TrpGlyPheArgGluGluLeuAlaProLeuValGlyProThrIleuTrpArgLeuGlnAsp 427  
DB 483 TGGGGGTTTCAGGAGGAATTTACACCCCTAGTGGGGCAACGCTTTGGGCACTCCAAAT 542  
QY 428 AlaProGlyThrProAlaIleAlaTrpGlyGluValProArgHisGlnLeuArgG 447  
DB 543 GCGCTTCCAGGAGCCCGCCATAGCTGGGAGAGGTCCCAAGGCCCGCTTCCAGT 602  
QY 447 yHisLeuThrHisTyrThrLeuCysAla---GlnSerGlyThrSerProSerValCysMe 466  
DB 603 CCACCTCACCCTACTACACCT-TGTGCCGATCGAAGTGGAAACCCCGCC-----CT 652  
QY 466 tAsnValSerGlyAsnThrGlnSerValThrLeuProAspLeuProTrpGlyProCysG 486  
DB 653 CCCCCCTGCATAAACCCCAATGTAATATCTCCCAATGCC-----CCCTTCTC 706  
QY 486 uLeuTrpValThrAlaSerThrIleAlaGlyGlnGlyProGlyProIleuArgIle 506  
DB 707 GACCTTCCCTTCCAGCCGCCCGGATACCGCCAGTCCGGACCCCGCCCACTCTG----- 761  
QY 506 uHisLeuProAspAsnThrLeuArgTrpLysValLeuProGlyIleLeuPheLeuTrpG 526  
DB 762 -----TCCCACTCTACTGGGCGCCCTT----- 785  
QY 526 yLeuPheLeuLeuGlyCysGlyLeuSerIleuAlaThrSerGlyArgCysTyrHisLeuAr 546  
DB 786 -----TTGTAACA-----TATCCACAACG 805  
QY 546 qHisLysValLeuProArgTrpValTrpGluLysValProAspProAlaAsnSerSerSe 566  
DB 806 C-----CCCTATTCTT----- 818  
QY 566 rGlyGlnProHisMetGluGlnVal-----ProGluAlaG 578

DB 819 -----CACCCACACCTCTCTCTCCCTTTGCTGTACTTCCATAGTTGACCCATCC 874  
QY 578 nProLeuGlyAspLeuPro-IleLeuGluValGluMetGluProProValMet- 597  
DB 875 CCCATTATCTGTATACCAGCCGCCCTCCCATATATAGACACCCCACTATAGTAC 934  
QY 598 -----GluSerSerGlnProAlaGlnAlaThrAlaProLeuA 610  
DB 935 TATGATAACCCCGCCCACTCGAATATTACGCCCCCACCACCACTGCTACCCCATCC 994  
QY 610 spSerGlyTyrGluLysHisPheLeuProThrPro 621  
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LOCUS 603062945F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212139 5',  
DEFINITION mRNA sequence.  
ACCESSION BI905856  
VERSION BI905856.1 GI:16168451  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 731)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1532 row: j column: 12  
High quality sequence stop: 731.  
Location/Qualifiers  
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/clone\_lib="NIH\_MGC\_118"  
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 9 6e-73 Length: 731  
Score: 1065.00 Matches: 216  
Percent Similarity: 93.94% Conservative: 1  
Best Local Similarity: 93.51% Mismatches: 5  
Query Match: 30.45% Indels: 10  
DB: 4 Gaps: 1

US-10-088-950A-1 (1-636) x BI905856 (1-731)

QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeuLeu 20



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Db 56 ATGGCGGAGGCTGGTGGCGCCCTTTCTGGCTGTGGCGCTGCCAAGCTGGCGCTCTG 115
Qy 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAla---GlyProLeu 39
Db 116 CCTCTGTTGGTGCTTTCCAGGAGGAGCGGTCCCGCAGT-ACAGCGCTGGGCGCACTG 174
Qy 40 GlnCysTyrGlyValGlyProLeuGlyAspLeuAnCysSerTrpGluProLeuGlyAsp 59
Db 175 CAGTGCTACGAGTGGACCCCTTGGCGACTTGAACCTGCTGCTGGGAGCTCTTGGGGAC 234
Qy 60 LeuGlyAlaProSerGluLeuHisGlnSerGlnLysTyrArg-SerAnlysThrG1 79
Db 235 CTGGAGGCCCTCCGAGTTACACCTCAGAGCCAAAGTACCTGTTCACAAACCA 294
Qy 79 nThrValAlaValAlaAla-GlyArgSerTrpValAlaLalleProArg-GluGlnLeuThr 98
Db 295 GACTGTGGCAGTGGCGGCTGGAGCGGCTGGGTGGCCATTCCTCTGTGGACACTCAC 354
Qy 99 MetSerAspLysLeuLeuValTrpGlyThrLysAla-GlyGlnProLeuTrpProVa 118
Db 355 ATGTCGACAACTCCTTGTCTGGGCGACTAAGGCAGTGCAGCCTCTCTGGCGCCCGT 414
Qy 118 lPheValAsnLeuGlnThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAs 138
Db 415 CTTCGTGAACCTAGAAACCCAAATGAAGCCAAACGCCCGCGCTGGGCGCTGACGTGGA 474
Qy 138 pPheSerGluAspAspProLeuGluAlaThrValHisTrpAlaProProThrTrpProSe 158
Db 475 CTTTTCCAGAGTACCCCTGGAGGCGACCTGTCATTTGGGCGCCACCTACATGGCCATC 534
Qy 158 rHisLysValLeuIleCysGlnPheHisTyrArgCysGlnGluAlaAla-TripThrL 178
Db 535 TCATAAAGTCTGATCTGCCAGTTCACACTCCGAGATGTCAGGAGCGGCGCTTGGAGCG 594
Qy 178 euLeuGluPro-GluLeuLysThrIleProLeu-ThrProValGluIleGlnAspLeuG1 197
Db 595 TGCTGGAACTGGAGCTGAAGACCATACCCCTGTACCCCTGTTGAGATCCAAAGATTGGA 654
Qy 197 uLeuAlaThrGlyTyrLysValTyrGlyArgCysArgMetGluLys-GluGluAspLeuT 217
Db 655 GCTAGCCACTGGCTACAAAGTGTATGGCCGCTGCCGATGGAGAAACGAAAGAGATCTGT 714
Qy 217 rpGlyGluTrpSerPro 222
Db 715 GGGCGAGTGGAGCCCC 731

RESULT 12
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LOCUS 602432807F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4550593 5',
DEFINITION mRNA sequence.
ACCESSION BG332437
VERSION BG332437.1 GI:13138875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
NIH-MGC http://imgc.ncbi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI243 row: n column: 02

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FEATURES
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                        /db_xref="taxon:9606"
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                        /tissue_type="large cell carcinoma"
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                        /clone_lib="NIH_MGC 18"
                        /vector="pOTB7; Site 1: XhoI; Site 2:
                        EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                        into EcoRI/XhoI sites using the following 5' adaptor:
                        GGCACAG(G). Library constructed by Ling Hong in the
                        laboratory of Gerald M. Rubin (University of California,
                        Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                        Superscript II RT (Life Technologies). Note: this is a
                        NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:          6,01e-72          Length:          942
Score:              1057.00           Matches:         220
Percent Similarity: 92.86%            Conservative:    1
Best Local Similarity: 92.44%          Mismatches:     13
Query Match:        30.22%            Indels:         8
DB:                  4                Gaps:          1

US-10-088-950A-1 (1-636) x BG332437 (1-942)
Qy 397 SerAlaSerGlyLeuAlaSerAlaSerSerValTrpGlyPheArgGluGluLeuAlaPro 416
Db 2 TCTGCTTTCAGGCTTGGCTCTGCATCTCTCGTCTGGGGTTTCAG-GAGGAATTAGCACCC 60
Qy 417 LeuValGlyProThrLeuTrpArgLeuGlnAspAlaProProGlyThrProAlaIleAla 436
Db 61 CTAGTGGGGCCACCGCTTTGGCGACTCCAAGATGCCCTCCAGGACC-CGCCGCATAGCG 119
Qy 437 TrpGlyGluValProArgHisGlnLeuArgGlyHisLeuThrHisTyrThrLeuCysAla 456
Db 120 TGGGAGAGGTCCCAAGGCCACAGCTTCGAGGCCACCTACCCACTACACCTTGTGTGCA 179
Qy 457 GlnSerGlyThrSerProSerValCysMetAsnValSerGlyAsnThrGlnSerValThr 476
Db 180 CAGAGTGGAAACACGACCCCTCCGCTCGCATGAATGTGAGTGGCAACACACAGAGTGTCA 239
Qy 477 LeuProAspLeuProTrpGlyProCysGluLeuTrpValThrAlaSerThrIleAlaGly 496
Db 240 CTGCCTGACCTTCTTTGGGGTCCCTGTGAGCTGTGGGTGACAGCATCTACCATCGCTGGA 299
Qy 497 GlnGlyProGlyProIleLeuArgLeuHisLeuProAspAsnThrLeuArgTrpLys 516
Db 300 CAGGGCCCTCCTGTGTCCTCCATCTCCGGCTTCATCTACAGATAACACCTTGAGGTGAAA 359
Qy 517 ValLeuProGlyIleLeuPheLeuTrpGlyLeuPhe-LeuLeuGlyCysGlyLeuSerLe 536
Db 360 GTTCTCCCGGACATCTATTCTTGTGGGGCTGTTCCTCTTGGGGTGGCCCTGAGCCT 419
Qy 536 uAlaThrSerGlyArgCysTyrHisLeuArgHisLysValLeuProArgTrpValTrpG1 556
Db 420 GGCACCTCTGGAAAGGTGTACCACTTAAGGCCAAAGTGTCTGCCCGCTGGGTCTGGGA 479
Qy 556 uLysValProAspProAlaAsnSerSerGlyGlnProHisMetGluGlnValProG1 576
Db 480 GAAAGTTCCTGATCTCCCAACAGCAGTTCAGGCCAGCCCCACATGGAGCAAGTACTGA 539
Qy 576 uAlaGlnProLeuGlyAspLeuProIleLeuGluVal---GluGluMetGluProPro 595
Db 540 GGGCCAGCCCTTGGGGA--CTTGCCATCTTGAAGTGGAGGAGAGATTTGGGGCCCCGCC 597
Qy 595 oValMetGlu-SerSer-GlnProAlaGlnAlaThrAlaProLeuAspSerGlyTyrGlu 614
Db 598 GGTATTGGAGGTCTCTCCCGAGCCGCCCGCCAGTGCCACGCCGCTTGACTCTGGGTATGAG 657

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found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 435.

# FEATURES

Location/Qualifiers

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/note="Organ: mixed; Vector: pYX-Asc; Site: 1: EcoRI;

Site 2: NotI; Library is oligo-dT primed and directionally

cloned. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated with

EcoR I adaptor, digested with Not I and then cloned

directionally into pYX-Asc vector. Average insert size

0.5-1kb. Adaptors 5' (AATTCGGCAGG)3' and 5'

(CTCTGCGCG)3'. 3' linker sequence - GCGCGCTGAGAGCC T18.

Sequencing primers 3' end: T3 promoter primer 5'd

(ATTAACTCTCAATAGGGA)3'. 5' End: T7 promoter primer 5'd

(TTATACGCTCACTATAGG)3'. Library was constructed in the

laboratory of M. Bento Soares. Average insert size 3-4kb

Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:

Pred. No.: 7,93e-67 Length: 803

Score: 990.00 Matches: 194

Percent Similarity: 93.27% Conservative: 0

Best Local Similarity: 93.27% Mismatches: 13

Query Match: 28.30% Indels: 3

DB: 7 Gaps: 0

US-10-088-950A-1 (1-636) x CF785854 (1-803)

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 QY 189 ThrProValGluIleGlnAspLeuGluLeuAlaThrGlyTyrLysValTyrGlyArgCys 208  
 DB 84 ACCCTCTGTGAGATCCCAAGATTGGAGCTAGCCACTGCTACAAAGTGATGCGCGTGC 143  
 QY 209 ArgMetGlnLysGluGluAspLeuTyrGlyLysThrPseerProIleLeuSerPheGlnThr 228  
 DB 144 CGGATGGAGAAGAAGAGGATTGTGGGGCGAGTGGAGGCCCAATTTTGTCTTCCAGACA 203  
 QY 229 ProProSerAlaProLysAspValTropValSerGlyValAsnLeuCysGlyThrProGlyGly 248  
 DB 204 CCGCTTCTCTCTCAAAAGATGTGTGGTATCAGGGAACCTCTGTGGAGCGCTGGAGGA 263  
 QY 249 GluGluProLeuLeuLeuTyrLysAlaProGlyProCysValGlnValSerTyrLysVal 268  
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 QY 269 TrpPheTrpValGlyGlyArgGluLeuSerProGluGlyIleThrCysCysSerLeu 288  
 DB 324 TGGTTCCTGGGTGGAGGTCGTGAGCTGAGTCCAGAGGAATTACCTGCTGCTCCTCA 383  
 QY 289 IleProSerGlyAlaGluTropAlaAArgValSerAlaValAsnAlaThrSerTrpGluPro 308  
 DB 384 ATTCACAGTGGGGAGTGGGCGAGGCTGTCCGCTGTCAACGCCACATCTGGGAGCCT 443  
 QY 309 LeuThrAsnLeuSerLeuValCysLeuAspSerAlaSerAlaProArgSerValAlaVal 328  
 DB 444 CTCACCAACCTCTCTTTGGTCTGTGGATTACGCTCTGCCCGCCCTAGCGTGGCATTC 503  
 QY 329 -SerSerIleAlaGlySerThrGluLeuLeuValThrTrpGlnProGlyProGlyGluPr 348

Db 504 ATCCAGCATCGCTGGGAGCAGGAGCTACTGTGACTGACACACAGGCGCTGGGAACC 563  
 QY 348 oLeuGluHisValValAspTropAlaArgAspGlyAspProLeuGluLysLeuAsnTrpVa 368  
 Db 564 ACTGGAGCATGTAGTGGACTGGCTCGAAT-GGTGACTCTCTGTATATATCTCAAGT-GT 621  
 QY 368 lArgLeuProProGlyAsnLeu 375  
 Db 622 CCGGTTTCTCTCTGGGTATCTC 643  
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 UI-HF-BK0-aay-b-06-0-UI-s1 NIH\_MGC\_36 Homo sapiens cDNA clone  
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 ACCESSION  
 AW575269  
 VERSION  
 AW575269.1 GI:7246808  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 570)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 AUTHORS  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE  
 Unpublished (1999)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. Tissue Procurement: Louis M.  
 Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Sequencing by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward  
 POLYA=No.  
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 /clone\_lib="NIH MGC 36"  
 /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 8.5e-65 Length: 570  
 Score: 961.00 Matches: 172  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 27.47% Indels: 0  
 DB: 2 Gaps: 0  
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 QY 1 MetArgGlyGlyArgGlyAlaProPheTrpLeuTrpProLeuProLysLeuAlaLeu 20  
 Db 55 ATGCGGGAGGAGGAGGCGGCGCTTTCTGGCTGTGGCGCTGCCAAGCTGGGCGCTG 114  
 QY 21 ProLeuLeuTrpValLeuPheGlnArgThrArgProGlnGlySerAlaGlyProLeuGln 40

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Db      115  CCTCTGTTGGGTGCTTTTCCAGCGGACGCGCTCCCGAGGGGAGCGCCGGGGCCACTGCAG 174
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Db      175  TGTACGGAGTTGGACCTTTGGCGACTTGAACCTGCTGCTGGAGGCTCTTTGGGGACCTG 234
QY      61   GlyAlaProSerGluLeuHisLeuGlnSerGlnLysTyrArgSerAsnLysThrGlnThr 80
Db      235  GGAGCCCCCTCCGAGTTACACCTCCAGAGCCAAAAGTACCGTTCCAACAAAACCCAGACT 294
QY      81   ValAlaValAlaAlaGlyArgSerTyrValAlaAlaProArgGluGlnLeuThrMetSer 100
Db      295  GTGGCAGTGGCAGCGGAGCGAGCTGGGTGGCCATTCTCTCGGGACAGCTCACCATGTCT 354
QY      101  AspLysLeuLeuValTyrGlyThrLysAlaGlyGlnProLeuTyrProValPheVal 120
Db      355  GACAAACTCTCTGTGGGGCACTAAGGCAGGCCAGCCTCTCTGGCCCCCGTCTTCGKG 414
QY      121  AsnLeuGluThrGlnMetLysProAsnAlaProArgLeuGlyProAspValAspPheSer 140
Db      415  AACCTAGAAACCAATGAAGCCAAACGCCCCCGCTGGGCCCTGACGTGGACTTTTCC 474
QY      141  GluAspProLeuGluAlaThrValHisTyrAlaProProThrTyrProSerHisLys 160
Db      475  GAGGATGACCCCTGGAGGCCACTGTCCATTGGGGCCCACTACATGGGCATCTCATAAA 534
QY      161  ValLeuLeuCysGlnPheHisTyrArgArgCysGln 172
Db      535  GTTCTGATCTGCCAGTTCCACTACCGAAGATGTCAG 570
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Search completed: February 23, 2005, 08:54:03  
Job time : 5431 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2005, 01:09:57 ; Search time 137 Seconds  
(without alignments)  
1519.163 Million cell updates/sec

Title: US-10-088-950A-1  
Perfect score: 3498  
Sequence: 1 MRGGRGAPFWLWPLKALL.....FLPTPEELGLLGP RPQVLA 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	15	US-10-351-157-9 Sequence 9, Appli
2	3498	100.0	636	15	US-10-352-554-9 Sequence 9, Appli
3	3498	100.0	636	16	US-10-755-889-164 Sequence 164, App
4	3494	99.9	636	10	US-09-791-497-14 Sequence 14, Appl
5	3494	99.9	636	13	US-10-000-776-12 Sequence 12, Appl
6	3494	99.9	636	16	US-10-777-790-12 Sequence 12, Appl
7	380	10.9	862	10	US-09-853-180-5 Sequence 5, Appli
8	331	9.5	861	15	US-10-398-666-12 Sequence 12, Appl
9	297.5	8.5	836	16	US-09-972-708-9 Sequence 9, Appli
10	297.5	8.5	836	16	US-10-659-295-34 Sequence 34, Appl
11	287.5	8.5	836	16	US-10-715-667-9 Sequence 9, Appli
12	288.5	8.2	970	15	US-10-351-157-135 Sequence 135, App
13	288.5	8.2	970	15	US-10-352-554-120 Sequence 120, App

14	277	7.9	837	16	US-10-659-295-35	Sequence 35, Appl
15	250	7.1	918	10	US-09-853-180-4	Sequence 4, Appli
16	250	7.1	918	10	US-09-972-708-8	Sequence 8, Appli
17	250	7.1	918	14	US-10-177-293-230	Sequence 230, App
18	250	7.1	918	15	US-10-295-027-74	Sequence 74, Appl
19	250	7.1	918	15	US-10-058-270A-32	Sequence 32, Appl
20	250	7.1	918	16	US-10-715-667-8	Sequence 8, Appli
21	248	7.1	708	14	US-10-313-135-2	Sequence 2, Appli
22	231.5	6.6	603	14	US-10-071-962-27	Sequence 27, Appl
23	226	6.5	979	10	US-09-972-708-7	Sequence 7, Appli
24	226	6.5	979	14	US-10-313-135-6	Sequence 6, Appli
25	226	6.5	979	15	US-10-351-157-7	Sequence 7, Appli
26	226	6.5	979	15	US-10-352-554-7	Sequence 7, Appli
27	226	6.5	979	16	US-10-715-667-7	Sequence 9, Appli
28	217.5	6.2	951	9	US-09-313-942-9	Sequence 9, Appli
29	217.5	6.2	951	9	US-09-935-868-9	Sequence 9, Appli
30	217.5	6.2	951	14	US-10-287-035-9	Sequence 9, Appli
31	217.5	6.2	951	14	US-10-282-162-9	Sequence 9, Appli
32	207	5.9	649	10	US-09-892-949-46	Sequence 46, Appl
33	207	5.9	649	15	US-10-351-157-109	Sequence 109, App
34	207	5.9	649	16	US-10-772-531-46	Sequence 46, Appl
35	207	5.9	662	10	US-09-972-708-15	Sequence 15, Appl
36	207	5.9	662	10	US-09-892-949-54	Sequence 54, Appl
37	207	5.9	662	14	US-10-006-265-17	Sequence 17, Appl
38	207	5.9	662	15	US-10-351-157-5	Sequence 5, Appli
39	207	5.9	662	15	US-10-352-554-5	Sequence 54, Appl
40	207	5.9	662	16	US-10-772-531-54	Sequence 15, Appl
41	207	5.9	662	16	US-10-715-667-15	Sequence 2, Appli
42	207	5.9	732	10	US-09-892-949-2	Sequence 11, App
43	207	5.9	732	15	US-10-351-157-111	Sequence 2, Appli
44	207	5.9	732	16	US-10-772-531-2	Sequence 6, Appli
45	206.5	5.9	1097	10	US-09-972-708-6	

ALIGNMENTS

RESULT 1  
US-10-351-157-9  
; Sequence 9, Application US/10351157  
; Publication No. US20030215838A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Gao, Zeren  
; APPLICANT: Kuijper, Joseph L.  
; APPLICANT: Dasovich, Maria M.  
; APPLICANT: Grant, Francis J.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Hammond, Angela K.  
; APPLICANT: No. US20030215838A1ak, Julia E.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Dillon, Stacey R.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
; FILE REFERENCE: 02-02  
; CURRENT APPLICATION NUMBER: US/10/351,157  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/435,361  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/389,108  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/350,325  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 636  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-351-157-9

Query Match 100.0%; Score 3498; DB 15; Length 636;  
Best Local Similarity 100.0%; Pred. No. 1e-256;





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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-164

Query Match      100.0%; Score 3498; DB 16; Length 636;
Best Local Similarity 100.0%; Pred. No. 1e-256;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGRGAPFWLWLPKLLALLPLWLFQRTPOGSAGPLOCYGVGPIGLDNCNWEPLGDL 60
Db 1 MRGRGAPFWLWLPKLLALLPLWLFQRTPOGSAGPLOCYGVGPIGLDNCNWEPLGDL 60
Qy 61 GASELHLOQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Db 61 GASELHLOQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Qy 181 PELKTIPLTVEIQDLELATGYKYGRCRMKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Db 181 PELKTIPLTVEIQDLELATGYKYGRCRMKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Qy 241 NLCGTPGGBEPLLLWKAPGCVQVSYKWFVWVGRELSPGIICTCCSLIPSGAEWARVSA 300
Db 241 NLCGTPGGBEPLLLWKAPGCVQVSYKWFVWVGRELSPGIICTCCSLIPSGAEWARVSA 300
Qy 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHVVDWARDGD 360
Db 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHVVDWARDGD 360
Qy 361 PLEKLNWRLPPGNLSALLPGNFTVGPYRITVAVSASGLASASSVWGFEELAPLVGP 420
Db 361 PLEKLNWRLPPGNLSALLPGNFTVGPYRITVAVSASGLASASSVWGFEELAPLVGP 420
Qy 421 TMLRLQDAPGPTAIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLD 480
Db 421 TMLRLQDAPGPTAIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLD 480
Qy 481 PWGCELVWTASTIAGGPPGPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
Db 481 PWGCELVWTASTIAGGPPGPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Db 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 4
US-09-791-497-14
; Sequence 14, Application US/09791497
; Publication No. US20030008343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Pfanz, Stefan
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
; FILE REFERENCE: DX010402
; CURRENT APPLICATION NUMBER: US/09791,497
; CURRENT FILING DATE: 2001-02-22
; PRIOR FILING DATE: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-497-14

Query Match      99.9%; Score 3494; DB 10; Length 636;
Best Local Similarity 99.8%; Pred. No. 2e-256;
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRGRGAPFWLWLPKLLALLPLWLFQRTPOGSAGPLOCYGVGPIGLDNCNWEPLGDL 60
Db 1 MRGRGAPFWLWLPKLLALLPLWLFQRTPOGSAGPLOCYGVGPIGLDNCNWEPLGDL 60
Qy 61 GASELHLOQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Db 61 GASELHLOQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKAGQPLWPPVFV 120
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Qy 181 PELKTIPLTVEIQDLELATGYKYGRCRMKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Db 181 PELKTIPLTVEIQDLELATGYKYGRCRMKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Qy 241 NLCGTPGGBEPLLLWKAPGCVQVSYKWFVWVGRELSPGIICTCCSLIPSGAEWARVSA 300
Db 241 NLCGTPGGBEPLLLWKAPGCVQVSYKWFVWVGRELSPGIICTCCSLIPSGAEWARVSA 300
Qy 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHVVDWARDGD 360
Db 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLHVVDWARDGD 360
Qy 361 PLEKLNWRLPPGNLSALLPGNFTVGPYRITVAVSASGLASASSVWGFEELAPLVGP 420
Db 361 PLEKLNWRLPPGNLSALLPGNFTVGPYRITVAVSASGLASASSVWGFEELAPLVGP 420
Qy 421 TMLRLQDAPGPTAIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLD 480
Db 421 TMLRLQDAPGPTAIAWGEVPRHQLRGHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLD 480
Qy 481 PWGCELVWTASTIAGGPPGPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
Db 481 PWGCELVWTASTIAGGPPGPIRLHLPLDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Db 541 RCYHLRHKVLPRVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVWNESS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 5
US-10-000-776-12
; Sequence 12, Application US/10000776
; Publication No. US20020164609A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pfanz, Stefan K.-H.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Rennick, Donna
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX010403
; CURRENT APPLICATION NUMBER: US/10/000,776
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
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; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 091627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 636
; TYPE: ERT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2433)..(2433)
; OTHER INFORMATION: Unidentified base.
US-10-000-776-12

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Query Match	99.9%; Score 3494; DB 13; Length 636;
Best Local Similarity	99.8%; Pred. No. 2e-256;
Matches 635; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MRGRGAPFWLWPLKLLP LLLWLFQRTRPQGSAGPLOCYGVGPLGDLNCSWEPLGDL 60
Db	1 MRGRGAPFWLWPLKLLP LLLWLFQRTRPQGSAGPLOCYGVGPLGDLNCSWEPLGDL 60
Qy	61 GAPSELHLOQKYSRNSKTQTVAAGRSWVAIPREQLTMSDKLLVMGTGKAGQPLWPPVFV 120
Db	61 GAPSELHLOQKYSRNSKTQTVAAGRSWVAIPREQLTMSDKLLVMGTGKAGQPLWPPVFV 120
Qy	121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPTWPSHKVLCQFHYRRCOEAAWTLLE 180
Db	121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPTWPSHKVLCQFHYRRCOEAAWTLLE 180
Qy	181 PELKTIPLTVEIQDLELATGYKYVGRCKMEKEEDLWGEWSPILSFOTPPSAKDVVWSG 240
Db	181 PELKTIPLTVEIQDLELATGYKYVGRCKMEKEEDLWGEWSPILSFOTPPSAKDVVWSG 240
Qy	241 NLGCTPGGEEPLLWKAGPCVQVSKVFWVGRELSPEGITCCCSLLISGAEWAWRSA 300
Db	241 NLGCTPGGEEPLLWKAGPCVQVSKVFWVGRELSPEGITCCCSLLISGAEWAWRSA 300
Qy	301 VNATSWEPNLNLSVCLDSASAPRSVAVSSITAGSTELLVWQPGPGPPLHHVVDWARDGD 360
Db	301 VNATSWEPNLNLSVCLDSASAPRSVAVSSITAGSTELLVWQPGPGPPLHHVVDWARDGD 360
Qy	361 PLEKLNWVRLPPGNLSALLPQNFTVGVYPYRITVTAVSASGLASASSVWGFRLELAPLVGP 420
Db	361 PLEKLNWVRLPPGNLSALLPQNFTVGVYPYRITVTAVSASGLASASSVWGFRLELAPLVGP 420
Qy	421 TLNRLQDAPGCTPAIANGVPRHQRLGHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLDL 480
Db	421 TLNRLQDAPGCTPAIANGVPRHQRLGHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLDL 480
Qy	481 PWGPCELWVTASTTAGCGPPGPIRLRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
Db	481 PWGPCELWVTASTTAGCGPPGPIRLRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
Qy	541 RCVHLRHKVLPRVWEKVPDANSSSQPHWEQVPEAQPIGDLPLLEVEEMEPVPMVMESS 600
Db	541 RCVHLRHKVLPRVWEKVPDANSSSQPHWEQVPEAQPIGDLPLLEVEEMEPVPMVMESS 600
Qy	601 QPAQATAPLDSGYEKHFLPTPEELGLLGP RPQVLA 636
Db	601 QPAQATAPLDSGYEKHFLPTPEELGLLGP RPQVLA 636

## RESULT 6

US-10-777-790-12  
; Sequence 12, Application US/10777790  
; Publication No. US20040198955A1  
; GENERAL INFORMATION:

QY 541 RCYHLRHVKVLRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMPPPPVMESS 600  
Db 541 RCYHLRHVKVLRWVWEKVPDPANSSSQPHMEQVPEAQPLGDLPLILEVEEMPPPPVMESS 600  
QY 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVPPQVLA 636  
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVPPQVLA 636  
RESULT 7  
US-09-853-180-5  
; Sequence 5, Application US/09853180  
; Publication No. US20030017617A1  
; GENERAL INFORMATION:  
; APPLICANT: Chirica, Madaline  
; APPLICANT: Parham, Christi L.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Moore, Kevin W.  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
; FILE REFERENCE: DX01074  
; CURRENT APPLICATION NUMBER: US/09/853,180  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/203,426  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 5  
; LENGTH: 862  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-180-5  
Query Match 10.9%; Score 380; DB 10; Length 862;  
Best Local Similarity 25.3%; Pred. No. 6.2e-20;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;  
QY 31 RPOGSAGPLOCYGVPLGDLNCSWEPLGD-----LGAPSELHLSQ----- 71  
Db 126 QPQN-----LSCIQKEGQVACTWGERGRDTHLYTEYTLQSLGPKNLTWQKQCDIYCDYL 181  
QY 72 -----KYRSNKTQV-AVAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFN 121  
Db 182 DFGINLTPESPESNFTAKVAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231  
QY 122 LETQMKPNAPRLGPDVSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWLTLEP 181  
Db 232 IKQ-KASVR-----CTLYWR-----DEGLVLLNLRYPNSRLNM----- 269  
QY 182 ELKTIPLTPV-----EIQDLELATGYKYGRCRMEKEEDLWGEWSPILSFQTP---PSAPK 234  
Db 270 ----VNVTKAKGRHDLDLKPFTEYEFQISKLHLKGSWDSSESLSRAQTPEEPTGML 325  
QY 235 DVWVSGNLCTPGCEEPILLWK-----APGCVQVSYKWFVWVGRELSPE--GITCCC 286  
Db 326 DVWYMKRHIDY-SRQQLISLFWKNLSVSEARGKILHYQVTLQELTGGKAMTQNTIGHTSWT 384  
QY 287 SLIPSGAEWA-RYSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWOP 343  
Db 385 TVIPRTGNWAVASAANSKSSULPTRINIMNLCAGLLAPQVANS-EGMDNLTWOP 443  
QY 344 ---GPGBLEHVVDWAR---DGDPLEKLNVRLLPGLNLSALLPQNFVTPYRITVAVS 397  
Db 444 PRKDPASAVQEVVWEWRELHPGGDTQVPLNLRSPYVNSALISENIKSYICYEIRVVALS 503  
QY 398 ASGLASASSVWGFEELAPLVGPTLWFLQDAPGTPPAIANGEVPRHQLRHLTHYLTC-- 455  
Db 504 GD-QGGCSSILGNSKHKAPLSGPHINAITE-EKGSILISWNSIPVQBMQCLLHYRYWK 561  
QY 456 -AOSGTSPSVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQPPGPIRLHLPDN 511  
Db 562 ERDNSQFQICEIPYRVSQNSHPINSIQ-PRVTYVLMWTALTATAGESHGNREFCI-QG 619  
QY 512 TLRWK--VLPFGI---LFLWGLFLGCGLSLATSRCYHLRHVKL-----PRWVWEKVP 559

Db 620 KANWMAFVAPSICIAIIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667  
QY 560 DRANSSSQPH-----MEQVPEAQPLGDLPLILEVEEMPPPPVMESSQPAQATA-----PLD 610  
Db 668 DRANSTCAKPIAIEKTLQPLDLRLLDWTFPE-----DPEPLVISEVLHVQVTPVFRHPPC 723  
QY 611 SGYEKHFPLTPEELGLLG-----PPRQVPL 635  
Db 724 SNWPQ-----REKGIQGHQASEKDMHMSASSPPPPREAL 756  
RESULT 8  
US-10-398-666-12  
; Sequence 12, Application US/10398666  
; Publication No. US20040073021A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOTECHNOLOGY RESEARCH AND DEVELOPMENT CORPORATION  
; TITLE OF INVENTION: CLONING AND SEQUENCING OF THE PORCINE INTERLEUKIN-12  
; FILE REFERENCE: 21419/92796  
; CURRENT APPLICATION NUMBER: US/10/398,666  
; CURRENT FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 861  
; TYPE: PRT  
; ORGANISM: Porcine sp.  
US-10-398-666-12  
Query Match 9.5%; Score 331; DB 15; Length 861;  
Best Local Similarity 25.0%; Pred. No. 3.2e-16;  
Matches 164; Conservative 83; Mismatches 263; Indels 146; Gaps 36;  
QY 31 RPOGSAGPLOCYGVPLGDLNCSWEPLGD-----LGAPSELHLSQ---KYRSNKT 78  
Db 126 QPQN-----VSCMQKGERGTVACSWDRGRDTHLYTAVTLQNLGPKNLTWQKQCDYCDSL 181  
QY 79 QTVAAGRSWVAIPRE-----QLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNA 130  
Db 182 DL-----GINLTPESPESSTYTAQTAINSL---GTASS---FPCTFTLLDV-VRLPL 226  
QY 131 PRLGPDVSEDDPLEATVHWAPPTWPSH-KVLIQCFHYRRQCEAAWLTLEPELKTPLT 189  
Db 227 PW---DIRK---CVNASVSTCTLQWRDEGLVLLNLRYPVYRSRWNVN---ATWAKG 277  
QY 190 PVEIQDLELATGYKYGRCRMEKEEDLWGEWSPILSFQTP---PSAPKDVWVSGNLCTGP 246  
Db 278 RHDVLDLKPFTEYEFQISKPHLQKGRWSDWSBSLRTQTPEKEPTGMLDVWYMKQHIDYK 337  
QY 247 GGEPEPLLMK-----APGCVQVSYKV-----WFWVGRELSPE 280  
Db 338 -ROOYLFWKNLSLSARGKILH--YQVTLQEVAGNATLQNTERNSTWT----- 386  
QY 281 GITCCCSLIPSGAEW-ARYSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTEL 337  
Db 387 -----IPRTGIMAAVASAANSKSSULPTRINIAIDLGAGLLAPQVANSANP-EGSDNL 437  
QY 338 LVTW-QPGBLEPL--BHVVDWAR---DGDPLEKLNVRLLPGLNLSALLPQNFVTPYR 391  
Db 438 LVKWTSPGEGATAVQEVVWEWRELHRLGGMQPPLSWLRSPPYNTSLISDNIPKICYEI 497  
QY 392 TWTAVASGLASASSVWGFEELAPLVGPTLWFLQDAPGTPPAIANGEVPRHQLRHLTH 451  
Db 498 RVHALSGD-QGGCSSIRGDLKHKAPLSGPHINAISE-EKGSILISWDEIPAQBMQCGILH 555  
QY 452 YTLG---AOSGTSPSVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQPPGPIRL 505  
Db 556 YRIYWERUSDQFQICEIPYRVSQNSHPINSIQ-PRVTYVLMWTALTATAGESPQGNERE 614  
QY 506 LHLPDNTLRWK--VLPFGI---LFLWGLFLGCGLSLATSRCYHLRHVKL-----PRWV 555

Db 615 FCL-QCKANWSTFVAPSICIAVITGVF-----SMRCFRQKVFVLLIALRPQWCS 663  
QY 556 EKVPDPANSSSQPH-----MQOVPEAQPLGDLPLILEVEEMPPPPVMESSQPAQAT 606  
Db 664 REIPDPANSTWAKKYPVIEKKQLSLDRLADWPTE-----EPPLVINEVLPOVT 715  
RESULT 9  
US-09-972-708-9  
; Sequence 9, Application US/09972708  
; Publication No. US2003005987A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Cosman, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: DuBose, Robert F.  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/09/972,708  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 9  
; LENGTH: 836  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-708-9

Query Match 8.5%; Score 297.5; DB 10; Length 836;  
Best Local Similarity 22.8%; Pred. No. 1.1e-13;  
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

QY 50 LNCSEPLGDLGAPSELHLQSKYRSN-KTQTVAV-----AAGRSWVAIPRQLTMSDKL 103  
Db 140 LICQWEPGPEHLPSTFTLSKFSKRGNCQTQDSILDVCPKDGQSHCCIPRKHLLYQNM 199  
QY 104 LVW-----GFKAGQPLW-----PPVFVNLETQMKNPAPRLG-----PDVDF 139  
Db 200 GIWVQNAENALGTSMSPQLCLDPMVVKLEPPMLRTMDPSPEAAPQAGCLQCWEP----- 255  
QY 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRRCQEAANTLLEPELKTIPLTVEIQDLEL 198  
Db 256 -----WQPLGHINQK-----CELHKPQGEASWALVGP-----LPLEALQVEL 294  
QY 199 -----ATGKVVYGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DVWVSGNLCGTPGGBE 250  
Db 295 CGLLPATAYTLQIRCIWRPLPGHWSWSPSLERLITRPTVRLDTW----- 341  
QY 251 PLLLLKAPGPCVQVSVKVFWVGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP-- 308  
Db 342 ---WRQ-----RQDPRTVQLFWKVPLEEDSGRIQGY-VVSWRPSG 379  
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSITAGST----- 335  
Db 380 QAGAILPLCNTTELCTFHLPSAEQVALVAYNSAGTSRPTPVFSESGRPALTRLHAMA 439  
QY 336 ----ELLVTWQPGCPGPELHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGVP 388  
Db 440 RDPHSLWGWEPNPNWPGQVYIEWGLGPPSASNSKNTWRMEQNGRATGFLLENIRPFQJ 499  
QY 389 YRITVTAVSAGSLASASSVWGFEELAPLVGPTLWRLQDAPPGTPTAIANGEVPRHLRGH 448  
Db 500 YEIIIVTPLYQDTMGPSQHVYAYSQEWAPSHAPEL-HLKHIGKTWAQLEWVWPEPELGKSP 558  
QY 449 LTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLDLPWGPCELW-----VTA 491  
Db 559 LTHYTIFTWNAQNQSFSAIILNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSTVLTL 616  
QY 492 STIAGOGPGPIRLHLPLDNTLRWLVPGILFWGLFLL---CGGLSLATSGRCVHLRHK 548  
Db 617 MTLTPEGS-----ELHI-----ILGLFGLLLLTCLCG-----TAWLCCSPNRK 655

QY 549 VLPRVWVEKVPDPANSSSG-----QPHMBQVP---EAQPLGDLPLILEVEEMPPPPVMS 599  
Db 656 ---NPLWPSVDPDPAHSSILGSVWPTIMEEDAQLPGLCTPPTIKTLVLEDEKPKVP-WES 711  
QY 600 SOPAQATAPLDSGVEKHFPLTPEELGLL-GPPR 631  
Db 712 HNSSETCG-----LPTLVQTVYVLQGDPR 734

## RESULT 10

US-10-659-295-34  
; Sequence 34, Application US/10659295  
; Publication No. US20040141946A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHNEIDER, ARMIN  
; APPLICANT: SCHAEBITZ, WOLFF-RUEDIGER  
; APPLICANT: KOLLMAR, RAINER  
; APPLICANT: SCHWAB, STEFAN  
; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC GRC  
; FILE REFERENCE: 229530US  
; CURRENT APPLICATION NUMBER: US/10/659,295  
; CURRENT FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US/10/331,755  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 34  
; LENGTH: 836  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-659-295-34

Query Match 8.5%; Score 297.5; DB 16; Length 836;  
Best Local Similarity 22.8%; Pred. No. 1.1e-13;  
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

QY 50 LNCSEPLGDLGAPSELHLQSKYRSN-KTQTVAV-----AAGRSWVAIPRQLTMSDKL 103  
Db 140 LICQWEPGPEHLPSTFTLSKFSKRGNCQTQDSILDVCPKDGQSHCCIPRKHLLYQNM 199  
QY 104 LVW-----GFKAGQPLW-----PPVFVNLETQMKNPAPRLG-----PDVDF 139  
Db 200 GIWVQNAENALGTSMSPQLCLDPMVVKLEPPMLRTMDPSPEAAPQAGCLQCWEP----- 255  
QY 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRRCQEAANTLLEPELKTIPLTVEIQDLEL 198  
Db 256 -----WQPLGHINQK-----CELHKPQGEASWALVGP-----LPLEALQVEL 294  
QY 199 -----ATGKVVYGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DVWVSGNLCGTPGGBE 250  
Db 295 CGLLPATAYTLQIRCIWRPLPGHWSWSPSLERLITRPTVRLDTW----- 341  
QY 251 PLLLLKAPGPCVQVSVKVFWVGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP-- 308  
Db 342 ---WRQ-----RQDPRTVQLFWKVPLEEDSGRIQGY-VVSWRPSG 379  
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSITAGST----- 335  
Db 380 QAGAILPLCNTTELCTFHLPSAEQVALVAYNSAGTSRPTPVFSESGRPALTRLHAMA 439  
QY 336 ----ELLVTWQPGCPGPELHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGVP 388  
Db 440 RDPHSLWGWEPNPNWPGQVYIEWGLGPPSASNSKNTWRMEQNGRATGFLLENIRPFQJ 499  
QY 389 YRITVTAVSAGSLASASSVWGFEELAPLVGPTLWRLQDAPPGTPTAIANGEVPRHLRGH 448  
Db 500 YEIIIVTPLYQDTMGPSQHVYAYSQEWAPSHAPEL-HLKHIGKTWAQLEWVWPEPELGKSP 558  
QY 449 LTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLDLPWGPCELW-----VTA 491  
Db 559 LTHYTIFTWNAQNQSFSAIILNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSTVLTL 616







Db 123 PPASPSNLSCLMHLTNSLVQWEPGPEETHLPSTFILKSFRRADCOYQSGTIPDCVAKK 182  
Qy 87 R-SWVAIPREQLTMSDKLLVW-----GTRAGQPLW--PPVFVNLETOMKPNAPRLGPD 136  
Db 183 RQNNCSIPRKNLLLYQYNAIWQAEENMLGSSPKCLDPMDVVKLEPPML-QALDIGPD 241  
Qy 137 VDFSEDDPLEATVHWAPTWPSHKVL--ICQFHYR-RCQEAATLL--EPBLKTIPLTPV 191  
Db 242 V--VSHQPGCLWLSWKP--WKPSYMEQCECELYQPLKGANWTLVFLHPSK-----DQF 293  
Qy 192 BIQDLELATGKYVYRCRMEKEEDLWGSPILSQTPPSAPK---DWWVSGNLCTPGG 248  
Db 294 ELGLHQAPVTLQMRCSRSLSPGFWSPWSPGLQRLPTMKAPTIRLDTWCQKKQL-DPGT 352  
Qy 249 EEPILLKAPGPCVQVSKVWFV-----GRELSPGEGIT--CCSLIPSGAEWARV 298  
Db 353 VSVQLFWK-PTPLQEDSQIOGYLLSNWSPDHQGDHLCNTTQLSCIFLPSAQ----- 407  
Qy 299 SAVNATSWEPITNLSVCLDSA--SAPRSV-----AVSSIAGSTE-----LLVTWQPG 344  
Db 408 -----NVTLVAYNKGATSSPTTVVFLNEGPAVTGLHAMAQDLNTIWDWEAP 455  
Qy 345 PGEPLHVVDWARDGDPLEK--LNNVRLPPGNLSA--LLPGNFTVGVYRITVAVSAGL 401  
Db 456 SLLPGYLIIEWEMSPSYNYSKSMWTEPNIGNITGLIKONINPQLYRITVAPLYGIV 515  
Qy 402 ASASSVWGFREELAPLVGP-----TLWLQDAPGTPAIANGVEPRHQLRGLHLYT 453  
Db 516 GPPVNVYTFAGERAPPAPALHLKHVGTWQAQLEWVPEAPL--GMIP-----LTHYT 566  
Qy 454 L-CAQSGT-SPSVCMVNGTQSVTLPLD--PWGPELWVTASTIAGO--GPEGPILRLHLP 509  
Db 567 IFWADAGHSFSTLNTIS--LHDFVLKHLBPASLYHYVLMATSRAGSTNSGLTLRLDP 624  
Qy 510 DNTLRWKVLPGLFLWGLFLGCGLSLATSRCYHLRHKVLPRWWEKVPDPANSS----- 565  
Db 625 SDL-----NIFGLICLVLLSTTCVVTWVWLCCKRRGKTS---FWSDDVPDPASHSLSSW 673  
Qy 566 -----SGQPHMEQVPEAQP-----LGDLPLIL---EVEEME 592  
Db 674 LPTIMTBETPOLPSFWDSSVPSITKITELEDKPKTHWDESSNGSLPALVQAYVLQGD 733  
Qy 593 PPPVWESSQAQATAPLDSGYEKHFLPTPEELG-----LLGPPRP 632  
Db 734 PREISNQSPSRTG--DOVLYGVLESPTSPPGMVQVIRSDSTQPLLGPTP 783

RESULT 15  
US-09-853-180-4  
; Sequence 4, Application US/09853180  
; Publication No. US20030017617A1  
; GENERAL INFORMATION:  
; APPLICANT: Chirica, Madaline  
; APPLICANT: Parham, Christi L.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Moore, Kevin W.  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
; FILE REFERENCE: DX01074  
; CURRENT APPLICATION NUMBER: US/09/853,180  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/203,426  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 918  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-180-4

Query Match 7.1%; Score 250; DB 10; Length 918;  
Best Local Similarity 20.5%; Pred. No. 4.9e-10;

Matches 133; Conservative 81; Mismatches 255; Indels 180; Gaps 22;  
Qy 119 FVNLET-----OMKPNAPRLGPDVDRSEDDPLEATVHWAPPTW 156  
Db 191 FVNIEVVEAENALGKVTSDHINFPDYKVKPNPH-NLSVINSEELSSILKLTWTWPSI 249  
Qy 157 PSHKVLICQFHYRCQBAAWTLLEPELKTIPLTPEIQLDELATGYKYVYRCRMEKEEDL 216  
Db 250 KSVIILKYNKYRKTADASTWSQIPPEDTASTRSFTVQDLKPFTEYVFRICMKEDGKG 309  
Qy 217 WGEHSP-----LSFQTPPSAPKDVVWSGNLCTPGGEEPLLWKAPGPCVQVSKVWFV 273  
Db 310 WSDMSEASGITVEDREDSKAPSFYKIDPSHTQGYRTVQLVWKTLP-----FEAN 360  
Qy 274 GRELSPEGITCCCSLIPSGAEWARVSAVNATSWEP-LTNLSL-----VCLDSASAPRSV 326  
Db 361 GKILDY-----VTLTRKSHLQNTVNTATKUTVNLNTDORYLATL 400  
Qy 327 AVSSIAGSTELLVTWQPGPELEHV-----VDWARDGDPLEK--LNNVRL 370  
Db 401 TVRNLVGKSDAAVLTIIPACDFQATHPVMDLKAPKPNMLWVETTPRESVKKYILENCVL 460  
Qy 371 -----PPGNL-SALLPGNFTVGVYRITVAVSAGLSASSVWGFREELAPL 417  
Db 461 SDKAPCITDQOEDGTVHRTYLRGNLAESKCYLITVTPVADGPGSPESIKAYLKQAPS 520  
Qy 418 VGPTLWRLQDAPGTPAIANGVEPRHQLRGLHLYTLCASGTSVCMVNGTQSVTL 477  
Db 521 KGFTV-RTKKVGKNEAVLEWDQUPVDVQNGFIRNYTIFRTIIGNETAVNVDSSTHTYL 579  
Qy 478 PDLFWGPELWVTASTIAGQGPPIRLRLHLP---DNTLRWKVLPGLFLWGLFLGCGL 534  
Db 580 SSLTSDTLVWVMAAYTDEGKGDPFTFTTPKFAQGEIEAIVVPVCL-----APLLTLL 635  
Qy 535 SLATSGRCYHLRHKVLPRWWEKVPDPANSSGQ--PH-----MEQVPEAQPLGDL 583  
Db 636 GVLF--CFNKR-DLIKKHIWPNVDPFSKSHIAQWSPTPPRHFNFSKQMYSDGNFTDV 691  
Qy 584 PILEVEBEMEP-----VMESSOPA----- 603  
Db 692 SVVEIENDKKPPEDLKSLLDFKKEKINTEGHSIGGSSCMSSSRPSISSDENESSQ 751  
Qy 604 -----QATAPLDSGYEKHFLPT-----PEELGLL 627  
Db 752 NTSSTVQYSTVHSGY-RHQVPSVQVFSRSESTQPLLDSEERPEDLQLV 799

Search completed: February 19, 2005, 01:20:02  
Job time : 140 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2005, 01:06:55 ; Search time 43 Seconds  
(without alignments)  
1423.113 Million cell updates/sec

Title: US-10-088-950A-1  
Perfect score: 3498  
Sequence: 1 MRGGRGAPFWLPLKALL.....FLPTPELGLGPPRPQVLA 636  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 JW0047	Class I cytochrome
2	298.5	8.5	783	2 JH0329	granulocyte colony
3	292	8.3	863	2 C3852	granulocyte colony
4	277	7.9	837	2 A3498	granulocyte colony
5	268.5	7.7	771	2 B38252	granulocyte colony
6	250	7.1	918	2 A36337	membrane glycoprotein
7	248	7.1	917	2 I49699	interleukin-130 -
8	226.5	6.5	918	2 A44257	leukemia-6 sign
9	206.5	5.9	1097	2 S17308	leukemia inhibitor
10	206	5.9	1092	2 JX0312	differentiation-st
11	178	5.1	894	1 A41527	protein-tyrosine k
12	170	4.9	1711	1 A55148	protein-tyrosine-p
13	164.5	4.7	1185	2 T46428	hypothetical prote
14	162.5	4.6	1197	2 T30581	neural cell adhesi
15	159	4.5	1825	2 C88400	protein H19W22.1 l
16	159	4.5	1825	2 T32828	hypothetical prote
17	155	4.4	942	2 S23251	protein-tyrosine k
18	154.5	4.4	880	2 B53743	protein-tyrosine k
19	151	4.3	1274	2 S55050	cardiac myosin-bin
20	151	4.3	1914	2 T42635	tenascin Y precurs
21	150	4.3	888	2 S23065	uto protein - mous
22	150	4.3	1232	2 T43037	neural cell adhesi
23	147.5	4.2	800	1 S31575	interleukin-4 rece
24	147.5	4.2	1239	1 A32579	neuroglian - fruit
25	146	4.2	876	2 I49152	protein-tyrosine k
26	146	4.2	1691	1 D54689	protein-tyrosine-p
27	144	4.1	890	1 A53743	protein-tyrosine k
28	144	4.1	1894	2 C54689	protein-tyrosine-p
29	143.5	4.1	4135	2 T42629	tenascin-X - bovin

30	142.5	4.1	1898	2 S46216	leukocyte antigen-
31	142	4.1	880	1 JC4166	protein-tyrosine k
32	141.5	4.0	1907	2 S50893	protein-tyrosine-p
33	140.5	4.0	862	2 T46289	hypothetical prote
34	140.5	4.0	1344	2 T14316	rig-i protein - mo
35	140.5	4.0	2302	2 T14328	protein-tyrosine-p
36	138.5	4.0	581	2 I45971	prolactin receptor
37	137	3.9	896	2 I56563	interleukin-3 rece
38	137	3.9	1257	1 A41060	neural cell adhesi
39	137	3.9	1259	2 A43425	Bravo/Nr-CAM cell
40	137	3.9	1268	1 A39640	neural cell adhesi
41	136	3.9	2944	2 A54849	collagen alpha 1(V
42	135.5	3.9	2222	2 T13924	sek protein - fru
43	135	3.9	3164	1 WMBEH6	UL36 protein - hum
44	134.5	3.8	1162	2 PC4184	leptin receptor, O
45	134.5	3.8	1742	2 S24600	projectin - fruit

ALIGNMENTS

RESULT 1  
JW0047  
Class I cytokinase receptor precursor - human  
N;Alternate names: WSX-1  
C;Species: Homo sapiens (man)  
C;Date: 17-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: JW0047  
R;Sprecher, C.A.; Grant, P.J.; Baumgartner, J.W.; Presnell, S.R.; Schrader, S.K.; Yamagi  
Biochem. Biophys. Res. Commun. 246, 82-90, 1998  
A;Title: Cloning and characterization of a novel class I cytokine receptor.  
A;Reference number: JW0047; MUID:98262921; PMID:9600072  
A;Accession: JW0047  
A;Molecule type: mRNA  
A;Residues: 1-636<SPR>  
A;Cross-references: UNIPROT:O60624; GB:AF053004; MID:g3153240; PIDN:AAC39755.1; PID:g315  
A;Experimental source: brain  
C;Genetics:  
A;Map position: 19p13.11  
C;Keywords: glycoprotein  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;515-540/Domain: transmembrane #status predicted <TM>  
F;554-561/Domain: cytoplasmic #status predicted <CTP>  
F;51,76,302,311,374,382,467/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 100.0%; Score 3498; DB 2; Length 636;  
Best Local Similarity 100.0%; Pred. No. 5.8e-229; Mismatches 0; Indels 0; Gaps 0;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRGGRGAPFWLPLKALLPLLVLFQRTTRPGSGAPLQCYGVGLDNLCSWEPLGDL 60  
Db 1 MRGGRGAPFWLPLKALLPLLVLFQRTTRPGSGAPLQCYGVGLDNLCSWEPLGDL 60

Qy 61 GAPSELHLSQKQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVMTGKAGQPLWPFV 120  
Db 61 GAPSELHLSQKQYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVMTGKAGQPLWPFV 120  
Qy 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLCQHYRRCQEAATLLE 180  
Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLCQHYRRCQEAATLLE 180  
Qy 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240  
Db 181 PELKTIPLTPVEIQDLLELATGYKVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240  
Qy 241 NLCGTGGEEPLLWAPGCPVQVSYKVMFWVGRELSPEGITCCCSLIPSGAEARVSA 300  
Db 241 NLCGTGGEEPLLWAPGCPVQVSYKVMFWVGRELSPEGITCCCSLIPSGAEARVSA 300  
Qy 301 VNATSHPELTNLSLVCLDSASAPRSVAVSIAGSTELLVTWQPGCEPLEHVVDWARDGD 360  
Db 301 VNATSHPELTNLSLVCLDSASAPRSVAVSIAGSTELLVTWQPGCEPLEHVVDWARDGD 360

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QY 361 PLEKLNWRLPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWGPREELAPLVGP 420
|||
Db 361 PLEKLNWRLPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWGPREELAPLVGP 420
|||
QY 421 TLWRLQDAPPGTPATAWGRVPRHQLRGLHLYTLCAQGSTSPSCMVNSGNTQSVTLPLD 480
|||
Db 421 TLWRLQDAPPGTPATAWGRVPRHQLRGLHLYTLCAQGSTSPSCMVNSGNTQSVTLPLD 480
|||
QY 481 PMGPCELWWTASTIAGQPPGPIRLHLPDNLTNRKWLPGILFLMGLFLLGGLSLATSG 540
|||
Db 481 PMGPCELWWTASTIAGQPPGPIRLHLPDNLTNRKWLPGILFLMGLFLLGGLSLATSG 540
|||
QY 541 RYHLRHKVLPRWWEKVPDPANSSSGQPHMVOPEAQPLGLDLPILVEEMEPVPMESS 600
|||
Db 541 RYHLRHKVLPRWWEKVPDPANSSSGQPHMVOPEAQPLGLDLPILVEEMEPVPMESS 600
|||
QY 601 OPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 601 OPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 2
JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JH0329; S21608
R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A;Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A;Reference number: JH0329; MUID:91079757; PMID:2147944
A;Accession: JH0329
A;Molecule type: mRNA
A;Residues: 1-783 <LAR>
A;Cross-references: UNIPROT:Q99062; GB:M59820; NID:g31698; PIDN:CAA39252.1; PID:g31699
A;Experimental source: placenta
A;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <M
F;25-627/Domain: extracellular #status predicted <EXT>
F;628-653/Domain: transmembrane #status predicted <TRA>
F;654-783/Domain: intracellular #status predicted <INT>
F;93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 8.5%; Score 298.5; DB 2; Length 783;
Best Local Similarity 23.5%; Pred. No. 1.9e-12;
Matches 164; Conservative 77; Mismatches 259; Indels 197; Gaps 34;

QY 50 LNCSEPLGLGAPSELHLQSKYRNS-KTQTVAV-----AAGRSWVAIPREOLTMSDKL 103
|||
Db 140 LIQWEPGPTHLPFTSLKSFKSGNCQIQGDSILDCVPKQDSHCCIPRKHLILYQNM 199
|||

QY 104 LVN-----GTRKAGQPLW-----PPVFVNLETKMPNAPRLG-----PDVDF 139
|||
Db 200 GIWVQAEALGTSWSPOLCLDPMVVKLEPPMLRTMDPSPEAAPPOAGCQLQWEP----- 255
|||

QY 140 SEDDPLEATHVWAPPWPSHKVLICQF-HYRRCQEAATLLEPELXITPLTPVEIQDLEL 198
|||
Db 256 -----WQPLGLHNOK-----CELRHKPQGEASWALVGP-----LPLEALQYEL 294
|||

QY 199 -----ATGKYVYGRCKMEKEEDLWGEWSPILSPQTSPAPK-----DVWVSGNLGCTPGGEE 250
|||
Db 295 CGLLPATAYTLQIRCIWRPLPGHSDWSPSLERLTTERTAPTVDLTWRQRQ-----D 348
|||

QY 251 P-----LLWKAAPGCVQVYKVFVWGGRELSPGITCCCLIPSGEAWARVSVAIVTSWE 307
|||
Db 349 PRIVQLEFWK-PVPLEEDSGRIQGV-----VSWRPSGQAGAILPLCNTTELS 394
|||

QY 308 PLTNL-----SLVCLDSA--SAPRSVAVSSITAGST-----ELLVTWQPGPG 346
|||
Db 395 CTFHLPSEAEVALVAVNSAGTSRPTVVFSESGPALTPLHWARDPSHLWGWGPPNP 454
|||

QY 347 EPLEHVVDWARDGDGFLEKLN--WVRLPPGNLSA-LLPGNFTVGVYRITVTAVSASGLAS 403
|||
```

```
Db 455 WPOQYVIENGGLGPPSASNSKNTWMEQNGRATGFLKKNIRPPQLYEIIIVTPLYQDMGP 514
|||
QY 404 ASSVWGFREELAPLVGPTLRQLDAPPGTPATAWGEVPRHQLRGLHLYTLCAQGSTSPS 463
|||
Db 515 SQHYAVYSQEMAPSHAPEL-HLKHGKTAQLEWVPEPPELGGKSPPLTHYTIFFWTAQNS 573
|||
QY 464 VCMNVSGNTQSVTLPLDLPWGPCELW-----VTASTIAGQPPGPIRL 506
|||
Db 574 FSATINASSRGFVLHGLE--PASLYHHILMAASQAGATNSTVLTMLTTEGS-----EL 626
|||
QY 507 HLPDNTLRKWLPGILFLMGLFLL-----GCGLSLATSRCYHLRHKVLPRWWEKVPDPAN 563
|||
Db 627 HI-----ILGLFGLLLLTCLCG-----TAMLCSPNRK---NPLWPSVPDPAH 667
|||
QY 564 SSSG-----QPMWEQVP-EAQPLGLDLPILVEEMEPV----- 595
|||
Db 668 SSLGSGWVPTIMEEDAFQPLGLGTPPTIKLTIVLEDEKKVPWESHNSSETCGLPTLVQTY 727
|||
QY 596 VMESQPAQATAP-LDSGYEKHFLPTPEELGLGPPR 631
|||
Db 728 VLQGDPRAVSTQPOSQSG-----TSDQ---AGPPR 754
|||

RESULT 3
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N;Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stimulat
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C;Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R;Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A;Title: Three different mRNAs encoding human granulocyte colony-stimulating factor recei
A;Reference number: A38252; MUID:91062348; PMID:1701053
A;Accession: C38252
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-863 <FUK>
A;Cross-references: UNIPROT:Q99062; GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; I
A;Note: clones pHG11 and pHG5
A;Accession: A38252
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-680,708-863 <FUK>
A;Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A;Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A;Reference number: JH0329; MUID:91079757; PMID:2147944
A;Accession: JH0330
A;Molecule type: mRNA
A;Residues: 1-680,708-863 <LAR>
A;Cross-references: GB:M59818; NID:g31696; PIDN:CAA39253.1; PID:g31697
A;Note: clone 25-1; Placenta
R;Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A;Title: Chromosomal gene organization of the human granulocyte colony-stimulating factor
A;Reference number: A46486; MUID:92091782; PMID:1530796
A;Accession: A46486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 855-863 <SET>
A;Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A;Experimental source: granulocyte
A;Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBIP:71485)
R;Hanu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A;Reference number: S68331; MUID:96132662; PMID:8554326
A;Accession: S68332
A;Molecule type: protein
```



A:Reference number: A38252; MUID:91062348; PMID:1701053

A:Accession: B38252

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-771 <FUK>

A:Cross-references: UNIPROT:Q99062; GB:M59819; GB:M38026; NID:g485363; PIDN:AAA63177.1;

Query Match 7.7%; Score 268.5; DB 2; Length 771;

Best Local Similarity 22.2%; Pred. No. 28-10;

Matches 146; Conservative 66; Mismatches 263; Indels 183; Gaps 30;

```
QY 50 LNCSEWPLGDLGAPSLHLSQSKYRSN-KTQTVAV-----AAGRSVAIPRQLTWSOKL 103
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 140 LICQWEPGETHLPSTFTLSKPSKRGNCQTQDGSILDCVPKDGQSHCCIPRKHLLYQNM 199
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 104 LVW-----GKAGQPLM-----PPVFVNLETOMKNAPRLG-----PDVDF 139
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 200 GIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPQAGCLOLCWEP---- 255
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 140 SEDDPLEATVWAPPTWPSHKVLIQCF-HYRRCQAAWTLLEPELKTITPLTVEIQDLLEL 198
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 256 -----WQPGHUIHOK-----CELRHKPQGEASWALVGP-----LPLEALQVEL 294
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 199 -----ATGYKVTGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DYWVSGNLCTPGGEE 250
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 295 CGLLPATATYLTQIRCIWRPLPGHWSDSPLSLRTTERTAPTVRLDTW----- 341
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 251 PLLWKAPGCVQVSYKVFVWGGRLSPGEGITCCCSLIPSGAEWARVSAVNATSWEP-- 308
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 342 ---WRQ-----RQLDERTVQLFWKVPLEEDSGRIQGY-VVSWRPSPG 379
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 380 QAGAILPLNCTTSLCTFHLPSAQEVALVAVNSAGTSRTPVVRSESGPALTRLHAMA 439
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 336 ----ELLVTWQPGFGBLEHVVDWARDGDPLEKLN--WVRLPPGNLSA--LLPGNFVTGVP 388
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 440 RDPHSLWGVWEPNPWPQGVVWGLGPPSASNSNKTWRMEQNGRATGFLKKENIRPFQL 499
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 389 YRTVTAVASGLASASSVWGFREELAPLVPTLWRLQDAPGTPALANGVPRQLRGH 448
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 500 YEIVTPLYQDTMGPSCHVYVAYSQEMAPSHAPL-HLKHGKTWAOLEWVPPPELKGSP 558
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 449 LTHYTLCAOSGTSFSCVMVSGNTQSVTLPLPWGPELW-----VTASTI--- 494
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 559 LTHYITFTWNAQNSFASILNASSRGFVLHGLE--PASLYHHLMAASOAGATNSVLT 616
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 495 -----AGCGPGPILRLHLPDNTLRWKVLPGLFGLGGLSLATSGRCVHLRH 547
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 617 MTLTAPTGRIPGQVSOITQL---TAAW--APGCPQSWRRMPPSCP-ALA-----RH 662
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 548 KVLPRWVWEKVPDPAOSSGQPMHQVPEAOPLGDLPILE--VEEMEPPVMESSOPA 603
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 663 PSPSSQCWRM--KRSRCPGSPITAQRPVAPSLWSPMCSRGTOEQFPSPNPPLAPA 718
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

## RESULT 6

A36337 membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004

C:Accession: A36337

R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MUID:91084844; PMID:2261637

A:Accession: A36337

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: UNIPROT:P40189; GB:M57230; NID:g186353; PIDN:AAAS9155.1; PID:g186354

C:Genetics:

A:Gene: GDB:1165T; GP130

A:Cross-references: GDB:126725; OMIM:600694

A:Map position: 5q11-5q11

C:Keywords: glycoprotein; membrane protein

F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 7.1%; Score 250; DB 2; Length 918;

Best Local Similarity 20.5%; Pred. No. 4.4e-09;

Matches 133; Conservative 81; Mismatches 255; Indels 180; Gaps 22;

```
QY 119 FVNLET-----QMKPNAPRLGPDVDFSEDDPLEATVHWAPTW 156
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 191 FVNIEVWEAENALGKVTSDHINFDPVYKVPKPNPH-NLSVINSEELSSILKLTWTNPSI 249
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 157 PSHKVLICQFHYRCQBAAWTLLEPELKTITPLTVEIQDLELATGYKYVYGRCKMEKEDL 216
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 250 KSVILKYNIOYRYKDASTWSQIIPEDTASTRSSTVQDLKPFTEYVYRIRCKMEDGKY 309
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 217 WGENSPI---LSQFPTSPAPKDVVWVGNLCOTPGGEBPLLLWKAPGCVQVSYKWFVWG 273
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 310 WSDWSEASGITIEDRPSKAPSFWKIDPSHTQGYRTVQLVWKTLP-----FEAN 360
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 274 GRELSPEGITCCCSLIPSGAEWARVSAVNATSWEP-LTNLSL-----VCLDSASAPRSV 326
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 361 GKILDYE-----VTLTRWKSHLQNYTVNATKLTNLTNDRYLATL 400
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 327 AVSISAGSTELLVTWQPGGEPLEHV-----VDWARDGDPLEK--LNWVRL 370
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 401 TVRNLVGKSDAAVLTIACDFQATHPVMDLKAFPKDNMLWVEWTPPRESVKKYILEWCVL 460
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 371 -----PPGNL--SALLPGNFTVGVYRITVTAVSASGLASASSVWGFREELAPL 417
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 461 SDKAPCIITDWOQEDGTVHRTYLRGNLAESKCYLITVTVYADGPGSPESIKAYLKQAPPS 520
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 418 VGPTLWRLQDAPPGTPALANGVPRHQLRGHLTHYTLCAOSGTSFSCVMVSGNTQSVTL 477
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 521 KGPTV-RTKVKGKNEAVLEWQDLPVDVQNGFIRNITFYRTIIGNEITAVNVDSHTEYTL 579
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 478 PDLWPGPCELWTASTITAGQPPGPIFLRLHLP---DNTLRWKVLPGLFLMGLFLGCGL 534
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 580 SSLTSDTLVYVMAAYTDEGKGDPFEFTTTPKFAQGEIAIVVPVCL---AELLTTL 635
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 535 SLATSGRCYHLRHKVLPRWVWEKVPDPAOSSGQ--PH-----MEQVPEAQPLGDL 583
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 636 GVLF---CFNKR-DLIKHHIWPVNPDPKSHIAQWSPTTPRPHNFNSKDMYSDGNFTDV 691
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 584 PILEVEEMEPPP-----VMESSOPA----- 603
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 692 SVVEIEANDKKFPFDDLKSLDLFKKEKINTEGSHGSGSCMSSSRFSISSDENESSQ 751
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 604 -----QATAPLDSGYEKHFLPT-----PEELGLL 627
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 752 NTSSTVQSVTVHSGY-RHQVPSVQVFSRSBSTOPLLDSEERPDLQLV 799
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

## RESULT 7

I49699

Glycoprotein 130 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C:Accession: I49699; I48370

R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.

J. Immunol. 148, 4066-4071, 1992

A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130.

A:Reference number: I48370; MUID:92291532; PMID:1602143

A:Accession: I49699

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: UNIPROT:Q00560; GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592

A:Accession: I48370

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>



A;Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817  
C;Genetics:  
A;Gene: gp130  
C;Keywords: glycoprotein  
F;134-314/Domain: cytokine receptor homology <CRS>

Query Match 7.1%; Score 248; DB 2; Length 917;  
Best Local Similarity 21.1%; Pred. No. 6e-09;  
Matches 140; Conservative 85; Mismatches 253; Indels 186; Gaps 27;  
Qy 107 GTKAGQPLWPPVFNLETKM-KPNAPRLG-----PDVDFSEDDPLEATVHAPP----- 154  
Db 177 GTSCWVSMPYYVNIWVEAENA--LGKVSSESIINFDVDRKPT-----PPNLSVTN 230  
Qy 155 -----TWPGHKV-----LICQHYRCQBAWTLLEPELKTIPLTPVEIQDLELA 199  
Db 231 SEELSSILKLSWSSGLGLDLKSDIQYTKDASTWIQVPLEDTMSPRTSFTVQDLKPF 290  
Qy 200 TGYKVGRCRMEKEEDLWGEWSPILS---FQTPPSAPKDVWVSGNLCTGPGGEEPLLLWK 256  
Db 291 TEYVFRIRSIKDSGKYMSDWSEASGTTYEDRSPRPSPFWYKTNPSHGQEYRSVRLWK 350  
Qy 257 APGPCVQVSVYK-----WFMVGGRELSPE-----GITCC 285  
Db 351 AL-PLSEANGKILDIYEVILQTSKVSQTYTGTGELTNLTNDRYVASLAARNKVGKSA 409  
Qy 286 CSL-IPSGAEWARYSAVNATSWPELTNLSLVC LDSASAPRSVAVSSITAGSTELLVTWQP 344  
Db 410 AVLTIPSHVTAAYSVVNLKAF-PKDNL-----LWVEWTPP 444  
Qy 345 PGEPLHVVDA---RDGDPLEKLNWRLPPGNLSALLPGNFTVGVPRITVAVSASGLA 402  
Db 445 PKPVSKVILENCVLSENAPCVE-DWQOEDATVNRTHLRGLLESKCYIITVTPVATGPG 503  
Qy 403 SASSVWGFREELAPLVGPTLWRLQDAPGTPAIAWGEVPRHQLRGLHLYTLCAQSGTSP 462  
Db 504 GSESLKAYLQQAAPARPTV-RTKKVGKNEAVLAWDQIPVDDQNGFIRNYSISYRTSVGK 562  
Qy 463 SVCNVSNGTQSVTLPLDPLMPGCPCLWVTASTIAGQGGPPGPIRLHLPL---DNTLRWKVLP 519  
Db 563 EMVHVDSSTHTYTLSSLSSTDLVWVMAAYTDEGGKDGPEFTTLPKPAQGEIAIVP 622  
Qy 520 GILPLWGLFLGCGLSLATSRCVHLRHKVLPWRWVEKVPDPANSSGQ---PH----- 570  
Db 623 VCL-----AFLTLTLGLVLF---CFNKR-DLIKKHWPVDPSPKSHIAQWSPHTPPRHNF 674  
Qy 571 --MEQVPEAQPLGDLPILEVEEMEPPP-----VMESSQP-----AQATAP--- 608  
Db 675 NSKDMYSDGNFTDVSVVEIEANNKPCPDDLKSVDLFKKVKVSTEGHSGIGSSCMSS 734  
Qy 600 SQP-----AQATAP-----LDSGYEKHFLPT-----PEE 623  
Db 735 SRPSISSNEENESAQSTASTVEYVTVHSGY-RHQVPSVQVFSRSESTQPLDSEERPED 793  
Qy 624 LGLL 627  
Db 794 LQLV 797

RESULT 8  
A44257  
interleukin-6 signal transducing molecule gp130 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A44257  
R;Wang, Y.; Nesbitt, J.E.; Puentes, N.L.; Fuller, G.M.  
Genomics 14, 666-672, 1992  
A;Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing  
A;Reference number: A44257; MUID:93052397; PMID:1427893  
A;Accession: A44257  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-918 <WAN>

A;Cross-references: UNIPROT:P40190  
A;Experimental source: liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:118488)  
C;Keywords: transmembrane protein  
F;134-315/Domain: cytokine receptor homology <CRS>

Query Match 6.5%; Score 226.5; DB 2; Length 918;  
Best Local Similarity 20.2%; Pred. No. 1.7e-07;  
Matches 130; Conservative 84; Mismatches 271; Indels 157; Gaps 23;  
Qy 105 VW-----GTKAGQPL-WPPVFNLETKMKNAPRLGPDVDFSEDDPLEATVHAPPWTW 156  
Db 195 VWVEAENALGNVSESEINFDV-----DKVKPPPH-NLSVTNSEELSSILKLAWNSSL 248  
Qy 157 PSHKVLICQHYRCQBAWTLLEPELKTIPLTPVEIQDLELATGYKVGRCRMEKEEDL 216  
Db 249 DSILRLKSDIQYTKDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIRSIKENGKY 308  
Qy 217 WGEWSPILS---FQTPPSAPKDVWVSGNLCTGPGGEEPLLLKAPGCPVQVSVYK----- 268  
Db 309 WSDWSEASGTTYEDRSPKAPSFYKVNANHPQEYRSARLIWKT-LPLSEANGKILDYEV 367  
Qy 269 -----WFMVGGRELSPEGITCCSLIPSGAEWARYSAVNATSWPELTNLSLVC 318  
Db 368 VLTQSKVSQTYTGTGELTN-----LTNRYVASLAARNVVGKSPATVLTIPGSH 419  
Qy 319 SASAPRSVAVSSITAGSTELLVTWQPGGEPLEHW-----DWARDGDPLEK 364  
Db 420 FKASHPVVDLKAPKONLLWVEWTP-PSKPVNKYILEWCVLSENSEPCIPDWQOEDGTNR 478  
Qy 365 LNWVRLPPGNLSALLPGNFTVGVPRITVAVSASGLASASSVWGFREELAPLVGPTLWR 424  
Db 479 TH-----LRGSLLESKCYLITVTPVPPGPGSPESMKAYLKQAAPSKGPTV-R 525  
Qy 425 LQDAPPGTPAIAWGEVPRHQLRGLHLYTLCAQSGTSPSCVMNVSGNTQSVTLPLDPWGP 484  
Db 526 TKKVGKNEAVLEMDHLFPVQNGFIRNYSISYRTSVGKEMVVRVDSHTYETLSLSSDT 585  
Qy 485 CELWVTASTIAGQGGPPG---ILRLHLPLDNTLRWKVLPGLPLWGLFLGCGLSLATSGR 541  
Db 586 LYMVMAAYTEGGKDGPEFTTLPKPAQGEIAIVVPVCL-----AFLTLTLGLVLF--- 638  
Qy 542 CVHLRHKVLPWRWVEKVPDPANSSGQ---PH-----MEQVPEAQPLGDLPILEVEE 590  
Db 639 CFNKR-DLIKKHWPVDPSPKSHIAQWSPHTPPRHFNFSKQMDYANFTDVSVVVEIEA 697  
Qy 591 MEPPP-----VMESSQP-----AQATAP--- 608  
Db 698 NNNKPCPDDLKSLDLFKKKEKISTEGHSGIGSSCMSSSRPSISSSEENESAQSTASTVQ 757  
Qy 609 ----LDSGYEKHFLPT-----PEELGLL 627  
Db 758 YSTVHSGY-RHQVPSVQVFSRSESTQPLDSEERPEDLQLV 798

RESULT 9  
S17308  
leukemia inhibitory factor receptor - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S17308  
R;Gearing, D.P.; Thut, C.J.; VandenBos, T.; Gimpe, S.D.; Delaney, P.B.; King, J.; Price,  
EMBO J. 10, 2839-2848, 1991  
A;Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 signal t  
A;Reference number: S17308; MUID:92007727; PMID:1915266  
A;Accession: S17308  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1097 <GEA>  
A;Cross-references: UNIPROT:P42702; GB:X61615; NID:934365; PIDN:CAA43805.1; PID:934366  
Query Match 5.9%; Score 206.5; DB 2; Length 1097;  
Best Local Similarity 19.5%; Pred. No. 4.8e-06;

Matches 138; Conservative 108; Mismatches 269; Indels 193; Gaps 37;

QY 47 LGDLNCSWEP--LGDLCAPSELHLSQKYSRKNKTQTVAAGRSWVAIPRE----- 95  
 Db 346 LKEIICSNPGRVTLVGP-----RATSYTLVESFGK-YRLKRAEAPTNESVQ 394  
 QY 96 ---QLTMSDKLLVWGTGAGQPL---WPPVFVNLETKMKNAPRLGPDVDFSDDDPLEAT- 148  
 Db 395 LLFQMLPQEIYNTLNANPLGRSOSTILVNIKEKYVHTP-----TSFKYKD-INSTA 448  
 QY 149 --VHMAPTWPSHKVLIQCFHYRRCOEAAWTLLEPELTKTIPTPVE-----IODLELATGY 202  
 Db 449 VKLSWHLPGNFAKINFLCEIIEIKNSV-----QEOBNVTIKGVENSYSVALDKLNEY 502  
 QY 203 KVTG-----RCMEKEEDLWGEW---PILSFQTPPSAPKDVWVSGNLCTGPGGEEPLLLWK 256  
 Db 503 TLYTFTRICSTETFWK-WSKWNSKKQHLTTEATSPSKGPDWTRE-----WSSDGKNLIYYK 557  
 QY 257 APGPCVQVSQVWVWVGRELSPEGITCCSLIPSGAEWAR-----VSAVNATS 305  
 Db 558 -PLPINEANGKILSY--NVSCSDEETQSLSEIPDPQHKAEIKLNDKNDYIISVAKNSVG 614  
 QY 306 WEFLTNLSLVCLDSASAPR-SVAVSSIAGSTE-LLVTWQPGPELEHVVDWARD--GDP 361  
 Db 615 SSPSKIA-----SMEIPNDLKIQVGVGKGIILLTHYDPMNTCDYVVIKWCNSRSRSP 669  
 QY 362 LEKLNWRLPPGNLSALLPGN-FTVGVPPYRITVAVSAGSLASASSVWGFRELAPLVCP 420  
 Db 670 C-LMDWRKVPNSNTEVIESDEFPRGIRYNFVLYGCRNOGYQLLRSIIGVYEE 728  
 QY 421 TLWRLQDAPGTPAIANGVEPRHQLRGLHLYTHYL-----CAQSGTSPSCVN 467  
 Db 729 N-FTVEDTSADSLVWEDIPVEELRGFLRGYLFYFGKGERDTSKRVLESGRSDIKVN 787  
 QY 468 VSGNTQ-SVTLPDLPWGPC-ELWVTASTIAGQGP-----GPILRLHLPDNTL 513  
 Db 788 ITDISQKTLRIADLQKTSYHLVLRAYTDCGVGPEKSMVVTWKENSAGLIILAIIP--V 844  
 QY 514 RWKVLPGILFLWGLFLGCGLSLATSGRCYHLRHKVLPWVWE---KVPDPAN----- 563  
 Db 845 AVAVIVGVW-----TSILCYRKR-----EWIKETFPDIPNENCKALOF 884  
 QY 564 -----SSSGOPHMEQVPEAQPLGDLPILEVEEMEP-- 593  
 Db 885 QKSVCEGSSALKTLEMNPCPNNVVEVLETSAPFKIEDTIIISPAERP-EDRSDAEPN 943  
 QY 594 -----PPVMESSQP-----AQATA-----PLDSGYEKHFLPTPEE 623  
 Db 944 HVVVSYPPIIEEIPNPADEAGGTAQVIYIDVQSMYOPQAKPEBEQ 991

RESULT 10  
 JX0312  
 differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text\_change 09-Jul-2004  
 C:Accession: JX0312; J02181; S88942  
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.  
 J. Biochem. 115, 557-562, 1994  
 A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.  
 A:Reference number: JX0312; MUID:94334302; PMID:8056772  
 A:Accession: JX0312  
 A:Molecule type: mRNA  
 A:Residues: 1-1092 <TOM>  
 A:Cross-references: UNIPROT:P42703; DDBJ:D26177; NID:g473718; PIDN:BAA05165.1; PID:d1008  
 A:Accession: J02181  
 A:Molecule type: mRNA  
 A:Residues: 1-717, 'EA' <TOM>  
 A:Cross-references: DDBJ:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494  
 A:Experimental source: liver  
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.  
 FEBS Lett. 334, 193-197, 1993  
 A:Title: Pregnancy associated increase in mRNA for soluble D-factor/LIF receptor in mouse

A:Reference number: S38942; MUID:94039833; PMID:7901054  
 A:Accession: S38942  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-717, 'EA' <TOM>  
 A:Cross-references: GB:D17444; NID:g441493; PIDN:BAA04258.1; PID:d1004778; PID:g441494  
 C:Keywords: differentiation; receptor; transmembrane protein  
 F:1-43/Domain: signal sequence #status predicted <SIG>  
 F:44-1092/Product: differentiation-stimulating factor/leukemia inhibitory factor receptor  
 F:828-854/Domain: transmembrane #status predicted <TM>

Query Match 5.9%; Score 206; DB 2; Length 1092;  
 Best Local Similarity 20.3%; Pred. No. 5.1e-06;  
 Matches 139; Conservative 93; Mismatches 256; Indels 198; Gaps 34;

QY 47 LGDLNCSWEP--LGDLCAPSELHLSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLL 104  
 Db 341 LKEIICSNPGRITGLVGP-----RNTETLFESISGKSAVFHRIEGLNTRYRL 390  
 QY 105 VMGTKAGO-----PL---WPPVFVNLETKMKNAPRLGPDVDFSDDDPLEATVH 150  
 Db 391 GVQHPGQEIHFNLITGRNPLGQAQSAVININTERVAPHDP---TSLKVKDINSIVTFTS 447  
 QY 151 WAPPTWPSHKVLIQCFHYRRCOEAAWTLLEPELTKTIPTPVE-----IODLELATGY 203  
 Db 448 WYLPNGFTKINLLCQIEICKANS-----KKEVRNATIRGAEDSTYHVAVDKLNPYATY 501  
 QY 204 VYGRCEKEEDLWGEWSP---ILSFQTPPSAPKDVWVSGNLCTGPGGEEPLLLWKAPGP 260  
 Db 502 FRVRC-SSKTFWKSRSWDEKRLHLLTTEATSPSKGPDWTRE-----WSSDGKNLIIVWK-PLP 555  
 QY 261 CVQVSYKQVWVWVGRELSPEGITCCSLIPSGAEWARVSAVNATSWEPLTN----- 311  
 Db 556 INEANGKILSY-----NVSCSL---NEETQSVLEI---FDPQHRAEIQLSKND 597  
 QY 312 --LSLVCLDSA-SAPRS-----VAVSSIAG-STEILLTWQPGPELEHVVDWA 356  
 Db 598 YIISVVAARNASGSSPPSKIASMEIPNDITVEQAVGLGNRIFLTWHRDPNMTCDYVVIKWC 657  
 QY 357 RD--GDPLEKNWRLPPGNLSALLPGN-FTVGVPPYRITVAVSAGSLASASSVWGFREE 413  
 Db 658 NSSRSEPC-LMDWRKVPNSNTEVIESDQFQGVRYNFYLGCTNOGYQLLRSIIGVYEE 716  
 QY 414 LAPLVGTLWRLQDAPGTPAIANGVEPRHQLRGLHLYTHYLCAQSGT----- 460  
 Db 717 LAPIVAPN-FTVEDTSADSLVWEDIPVEELRGFLRGYLFYFGKGERDTPKTRSLPEPH 775  
 QY 461 SPSVCMVSGNTQ-SVTLPDLPWGPC-ELWVTASTIAGQGP-----GPILRL 506  
 Db 776 SDIKLKNITDISQKTLRIADLQKTSYHLVLRAYTHGGLGPEKSMFVVVTKENSAGLIILAI 835  
 QY 507 HLPDNTLRWKVLPGLFLWGLFLGCGLSLATSGRCYHLRHKVLPWVWE---KVPDPA 562  
 Db 836 LIP---VAVAVIVGVW-----TSILCYRKR-----EWIKETFPDIPNPE 872  
 QY 563 N-----SSSGOPHMEQVPEAQPLGDLPILEVEEMEP-- 588  
 Db 873 NCKALQFQKSVCEGSSALKTLEMNPCPNNVVEVLETSAPFKIEDTIIISPAERP-GER 931  
 QY 589 EMEEP-----PPVMESSQP-----SQPA 603  
 Db 932 SEVDPENHVVSYPPIIEEITNPA 957

RESULT 11  
 A41527  
 protein-tyrosine kinase (BC 2.7.1.112) axl precursor, major splice form - human  
 N:Alternate names: transforming protein axl; UFO receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 28-May-1992 #sequence revision 05-Jan-1996 #text\_change 09-Jul-2004  
 C:Accession: A41527; B41527; E38269; I39203; G02782  
 R:O'Bryan, J.P.; Frye, R.A.; Cogswell, P.C.; Neubauer, A.; Kitch, B.; Prokop, C.; Espino  
 Mol. Cell. Biol. 11, 5016-5031, 1991

Qy	59	DLGAPSELH-LOSOKY---RSNKTQTVAAGR-----SWVAIPREQLTMSDKLLVWGKTGAG	111
Db	63	E-----PPEVHWRLDGQILLEADSTQT-QVPLGEDEQDDWIVVSQRLIT-----	105
Qy	112	QPLWPPVFNLETCMKENAPRLGDVDFSEDDPLEATVHVWAPTWSHKLVIQCFHYRRC	171
Db	106	-----SIQLSDTGYQCLV-----FLGHOTFVSQPGVYGL	135
Qy	172	QEAATLILPELKIPL-TPVEIQDLLELATGYKVYGRCMRKEBEDLWGEWSPILSFOTPP	230
Db	136	EGLPYFLEEEDRTVAANTFPNLS-----CQA-----QCPP	166
Qy	231	SAPKDVVSGNLCGTPGGEPLLLWKAPGCVQVSYKWFVWGGRELSPEGITCCCSLIP	290
Db	167	EPVDLLWL-----QDAVELATAPGHGPKQSLHV-----PGLNKTSSFCEAHNA	210
Qy	291	SGEAWRVSAVNATSWEPNLNLSVCLDSASAPRSVAVSSIASGTELLTWQGPFG-EP	348
Db	211	KGVTTGRTATITVLPOOP-RNLHLVSRQ-----PTELEVAMTPELCSGIYP	254
Qy	349	LEHVWDWA---RDG-----DPLEK-LNWVRLPPGNLSALLPGNFTVGVPYRITVTA	395
Db	255	LTHCTQLAVLSDDMGIQAGEPPPEPLTSQASVPHQLRL---GSLHPHTYHTRVAC	311
Qy	396	VSASGLASSVYMGFREELAPLVGPTLWRLQDAPGTPA-----IAWGE	439
Db	312	TSQGPSS---W-----THMLPVETPEGVPLGPPENISATRNGSQAFVHWQE	355
Qy	440	VPHQLRGHLTHYTLCAQSTSPSCVMVSGNTQSVTLP---DLPWGPCELTWTASTIAG	496
Db	356	-PRAPLQGTLLGYRLAYQGDTPEVLMDI-GLRQEVTELEQGGSGVSNLTVCAVAATAAG	413
Qy	497	QGP-----PGPILLRLHPDNTLRKVLPGILFLWGLFLIG-----CGLSLIA	537
Db	414	DGPWSLPVPLEAWRPPQAQPVH---QLVKEPSTPAFSWPNWYVLLGAVVAACVLILA	468

RESULT 12

A55148

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat

N;Alternate names: OST-PTP; oocyteesticular protein-tyrosine-phosphatase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: A55148

R;Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J. Biol. Chem. 269, 30659-30667, 1994

A;Title: Identification of a hormonally regulated protein tyrosine phosphatase

A;Reference number: A55148; MUID:95074080; PMID:7527035

A;Accession: A55148

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1711 <MAU>

A;Cross-references: GB:I36884

C;Comment: The sequence contains ten fibronectin type III repeats and two prote

C;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin typ

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmemb

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status pred

F;1174-1398/Domain: protein-tyrosine-phosphatase homology <PTPH>

F;1350/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 4.9%; Score 170; DB 1; Length 1711;

Best Local Similarity 21.3%; Pred. No. 0.0024;

Matches 138; Conservative 66; Mismatches 228; Indels 216; Gaps 33;

Qy	16	KLALLPLW-----VLFFQTRFGSAGPQCQGVGPGLDLNCWEPLDGLGAPSE-----	65
Db	107	KLTVLPCHQNVITITARTATTVVRG-IQLHSAGSPARLEASWS-----DAPGDQDSVQ	160
Qy	66	----LHLQSQKYSRN-----KTQTVAAAGRSWVAIPREQLTMSDKLLVWGKTGAGPLWPPVF	119
Db	161	LALLHLESQTLACNVSVSDTILSYSGFD---LLLEGTOYVL--EVITW---AGS-----	205

QY 120 VNLETOMKENAPRLGPDVDFSEDDPLEATVHVAPPTWPSHKVL----- 162  
 Db 206 LHAQTSI-----LQWTEVPDPDHLALRALGTSSLOAFWNSSEG 243  
 QY 163 ICQFYHRCQEAAT-----LLPELKT-----IPLTPVEIQDLELATGKYVYGRCRME- 211  
 Db 244 ATSFHMLTDLGGTWTAVIRQGVSTHTFLHLSPTGTHLKI CASAGPHQWGPSATEW 303  
 QY 212 -----KEEDLWGEW-----SPILSFOT-----P 229  
 Db 304 TYPSPDLVLTPLRNLWASWKAGLGARDGYVLKLSGPMESTSTLGPCECNAPFGPLP 363  
 QY 230 P-----SAPKDVWVSGNLCGTPGGBEPLLLWKAPGPCQVQSYKWFVWGGRELS- 278  
 Db 364 PGHYTLQLKLAGFYDAWVEGS---TWLAESAALPREVEFG-----ARLWLDGLEASK 412  
 QY 279 -----PEGIT---CCCSLIPSGAEWARVSANVATSWEPULNLSL 314  
 Db 413 QPGRALLYSDDAPSGLSNISVPSGATHVIFCLVP-GAHY-RVDIASGTG---DISQSI 467  
 QY 315 VCLDSASAPRSVAVSSIAGSTELLVTPQPGGEPLLEHVVDWARDGDPLEKLNWVRLPPGN 374  
 Db 468 SGYTSPLPQSLVLEISKSPSGLTIAWGPAGGLECYKVTWHDGSGRSPGDLVDLGPDT 527  
 QY 375 LS-----ALLPGNTVGVPRITVAVS-ASGLASASSVWGFEELAPLVGPTLWRLQDA- 428  
 Db 528 LSLTLKSLVPGS-----SYTWSAWAWAGNLGSDSKTHSCTRPA-----PTNLSLGFAH 577  
 QY 429 PPGTPALAMEGEVPRHQLRGLHLYTLCAOSGTPSPVMVSGNTQSVTLPLDLPWGPCELMW 488  
 Db 578 QPAAALKASWHPGGRDAFHLYRLRPLTLESEKV---LPREAQFNSWAQLTAG-CBEPQ 633  
 QY 489 VTASTI-----AGCGPGPIRLRLHPDNT-----LRKWLP 520  
 Db 634 VQLSTLWGSRRSSANATGTPPSAPTLVNVTSADPTQLQVSWAHVPG 681

RESULT 13  
 T46428  
 hypothetical protein DKFp434B2226.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
 C:Accession: T46428  
 R:Ansoorge, W.; Wirkner, U.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z23028  
 A:Accession: T46428  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1185 <AAA>  
 A:Cross-references: UNIPROT:Q9NTD2; EMBL:AL137357  
 A:Experimental source: adult testis; clone DKFp434B2226  
 C:Genetics:  
 A:Note: DKFp434B2226.1

Query Match 4.7%; Score 164.5; DB 2; Length 1185;  
 Best Local Similarity 20.3%; Pred. No. 0.0036;  
 Matches 120; Conservative 68; Mismatches 194; Indels 209; Gaps 27;  
 QY 96 QLTWMSDKLLVWGTKA-----GOPLWPPVFNLETOMK---FNAPRLGPDVDFSEDDPL 145  
 Db 231 QLTGLGKVIYEQVLAFTIRIGDGSHPPI---LELTLDVGPWM---GILFPEVRIT 284  
 QY 146 EATVHVAPPTWPSHKVLICQFHYR-----RCQEAATWLLPELKIPLTPVEIQDLEL--- 198  
 Db 285 SVRLIWQPPAAPNGIILAYQITHLRNTTANTATVEVLAPSARQYATATGLKPSVYLFRI 344  
 QY 199 -ATGYKYVGRCR-----MEKEEDL-----W----- 217  
 Db 345 TAQTRKWGEAAEALVVTTEKRRDPQPPSRPMWQEDVRARSVLLSWEPGSDGLSPVRY 404  
 QY 218 -----GEWS-----PILSFQTPPSAPKDVWVS-----G 240

Db 405 TIQTRPLSPGRWALHSASVSHNASSFIVDLRKPTSYKFRVKATNDIGDSEFSESESLT 464  
 QY 241 NLCTPGGEBPILL-----WKAPGPCVQVSYKWFVWGGRELSPEGIT---CC 285  
 Db 465 TLQAAP-DEAPTILSVTPHTTTSVLIRWQPPAEDKINGILLGFRIRYRELLYEGRLGFTL 523  
 QY 286 CSLIPSGAEWA-----RVSANVATSWEPULNLSL 313  
 Db 524 RGINNPGATWAELTSMYMRNLSPSLTYVELDNLNKHRYEIRMSYNAVGEFSPSPQ 583  
 QY 314 LVCLDSA---SAPRSVAVSSIAGSTELLVTPQPGGEPLLE---HVVDW-ARDGDPLE 363  
 Db 584 EVFGEAVPTAAPNVVHVG-ATATQDVTWEPPLDQSDIQQYKIYFEWAQRGNLTE 642  
 QY 364 KLNWVRLPPGNLSALLPCNFTVGVPRITVAVSASGLASASSVWGFEELAPLVGPTLW 423  
 Db 643 RVKTLFLAENSVKL---KNLTGYTAYMVSVAAFAAGDGPST-----PTQG 686  
 QY 424 RLQDAPGCTPA-----IAW--GBVPRHQLRGLHLYTLCAQ-SGTSPPSCMN 467  
 Db 687 QTOQAAAPASPSVKFSELTTTSVNVSWEARQFPNGILLEGYRLVYPCSPVDGVSKIITVD 746  
 QY 468 VSGNT-----QSVT-----LPDLPWGPCELMWVTAAGQPPGP 502  
 Db 747 VKGNSPLWLKVKDLAEGVTVYFRIRAKTFTYGP-EIEANVTTPGEGAPGP 796

RESULT 14  
 T30581  
 neural cell adhesion molecule L1.1 - zebra fish (fragment)  
 C:Species: Brachydanio rerio (zebra fish)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T30581  
 R:Tongiorigi, E.; Bernhardt, R.R.; Schachner, M.  
 J. Neurosci. Res. 42, 547-561, 1995  
 A:Title: Zebrafish neurons express two L1-related molecules during early axonogenesis.  
 A:Reference number: Z20875; MUID:96155762; PMID:8568941  
 A:Accession: T30581  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1197 <TON>  
 A:Cross-references: UNIPROT:Q90478; EMBL:X89204; NID:gl065713; PID:gl065714; PIDN:CAA614;  
 C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; in

Query Match 4.6%; Score 162.5; DB 2; Length 1197;  
 Best Local Similarity 22.0%; Pred. No. 0.005;  
 Matches 127; Conservative 80; Mismatches 212; Indels 159; Gaps 34;  
 QY 26 LFORTRPQGSAGPLQCYGVG-PLGLDNCWEPPLGDLGAPSELHLQSQYKRSNKTQTVAVA 84  
 Db 370 LYQAT--AGQTVMLDCRTFGSPLPKIH--WEILDSIPALSNAKISQTTNGSLKISNVSEE 425  
 QY 85 AGRSWAIPRE--QLTMSDKLLVWGTKAQQLWPPVFNLETOMKPNAPRLGPDV---D 138  
 Db 426 DSNRYTCVSVETNKSISADVEVLNRTKI---VGPP--QNLHVIR-----GSDAILHCK 473  
 QY 139 FSEDDPLEA-TVHWAPPTWPSHKVLIC---QFHYRRCQEAATWLLPELKIPLTPVEI 193  
 Db 474 YTVDNHLSKSPVQW---NKDGHKITASTSNKYHE---IEGSLKVLVDQMEDMGSIYCEV 527  
 QY 194 Q---DLELATGKYVYGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSGNLCGTPGEE 250  
 Db 528 STTLSDTSATSGY-----ITVQDKPDPQSLKLSKKN-----BRS 561  
 QY 251 PULLWKAPGPCVQVSYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP 308  
 Db 562 VTISWM---PSYENNSPVTEYV--IEMN-EGET-----PDEGQMKYRSVSQDIDSWRS 609  
 QY 309 LTNLS-----LVCLDSASAPRSVAVSSIAGST-----ELLVTW 341  
 Db 610 ICSYKYHFQIRAVNSIGTSAPTE---SLSYSVSTPAKPDTPNPNVMTLSTDPKSMIISW 666

Qy 342 QP-----GRGEPLHVVHARDGDDPLEKLNW-----VRLPPGNLSALLPQNFVGVDPYR 390  
Db 667 QEMDRROFNGFG--FOYKVFRRRAAD--SGAHWTSESSVSNPP-----LMVNNTGTFVSFE 717  
Qy 391 ITVTAVSASGLA-SASSVMGPRELAPLVGPTLWRLQDAPPTAIANGEVPRHQLRGHL 449  
Db 718 IKVQAVNDLGAAPLEPLTVIGSGDFLEAPSAUSVTELOKTSVMWRVSPVRPESVRGHL 777  
Qy 450 THYTLCAQSGTS-----PSVCNMVSGNTQSVTLP-----DLP-WGPCELWWTASTIA 495  
Db 778 LGYKIYLRMGKSQWETPGRAVSSSGNPTVIEVPADAAEKIVSDIQFYSDYTLTITAFNSK 837  
Qy 496 GQGP-----PGPIRLHL-----PDNTRLWK 516  
Db 838 GEGPHSEBSTPEGAGPVLFLPFDSPSESEITLRWE 875

RESULT 15  
C88400  
protein H19W22.1 [imported].. Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C88400  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; PMID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: C88400  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1825 <STO>  
A:Cross-references: UNIPROT:Q9UB28; UNIPROT:Q9UB29; GB:chr\_III; PIDN:AAB94997.1; PID:g27  
C:Genetics:  
A:Gene: H19W22.1  
A:Map position: 3

Query Match 4.5%; Score 159; DB 2; Length 1825;  
Best Local Similarity 21.2%; Pred. No. 0.015;  
Matches 128; Conservative 76; Mismatches 245; Indels 156; Gaps 32;

Qy 105 VMGTYK-----AGQPLMPPVFNLETKMKNAPR-LGPDVDVDSDDPLEATVHWAPPTWP 157  
Db 1 MWSVKIRAINSAHSATWPA---AQTKTPGGELIIGFDVSYRQCKPI---ISWRSKENT 54  
Qy 158 SHKVLICQFYHRCQEAATWILLEPELTIPLT-----PVEIQDLELATGYKVGRCRMEKE 213  
Db 55 NDLESFVLEWKSTESSW---RQHRNPIPYNGWQRFPYSVDLGPQGHYQVRI-VAKD 110  
Qy 214 EDLWGEW-SPILSPQT-----PPSAPKDVWVSGNLGCTPGGEPPLLWKAPGPC-VOVS 265  
Db 111 PNRCNATSPVQVQVOTOSQKAPRAPADVQS-----PL-----GPTQIRVQ 153  
Qy 266 Y-----KVMFWGRELSPGEGITCCCSLIPSGAEWARVAVNATSWEPFLTNLSL 314  
Db 154 WAPLHESEWNCRLWYIVKHSITPQNGF---KNLTNGENFVFDSDPYTQW---NFEV 205  
Qy 315 VLDSAS-----APRSVAVSSI---AGSTELLVWQPGGEPLEHVVDWAR 357  
Db 206 QAANPAGESOWSRAQSQATQGVAFGAVANLRVQIPGDSLQCSNQP-PVNPNGRITQY-- 262  
Qy 358 DGDPLEKLMVRLPPGNL--SALLPQGNFTVGPV-----YRITVAVSASGLAS 403  
Db 263 -----EVTQLISRGCDNNOEAPRTITVNGPHFTITGLPHSKYKRVGVAKENVGAGE 316  
Qy 404 ASSVMGPRELAPLVGPTLWRLQDAPPTAIANGEVPRHQLRGHLTHYTLCAQSG---- 459  
Db 317 RVSLIEIQDQAAPSGAPLYLRTEDIRFTDVSISMQAPPCLTNGEITEYEYEVTAGDRRQ 376  
Qy 460 TSPSVCMNVSG-----NTQSVTLDDL-----WGPCELWWTASTIAGO---GPPGP 502  
Db 377 TVQKTTENIRGTRAKIENLOPQTRYNVKVRAYTARGAGPWSDEVFPQTSAGQQNVQAPGF 436

Qy 503 ILRLHL-PDNT-LRWK---VLPGLFLWGLFLGCGLSLATSRCYHLRHKVLPRLRWWEK 557  
Db 437 VKVLHTGADNAQLVWQSPYVNPVGV-----DKYKCRVAPSGTQOYQE 478  
Qy 558 VPDPAANSSSQPHMEQ--VPEAQPLGDLPLILEVEEMEPVPPVMESSQPAQATAPL-DSGYE 614  
Db 479 RQFPFAVSPCCOQRIERQNLQSPFGSLHCGRIENLRP-----EQTYDFQVSAHVKDSGWG 534  
Qy 615 KHFLP 619  
Db 535 PYSPP 539

Search completed: February 19, 2005, 01:16:51  
Job time : 47 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 19, 2005, 01:06:05 ; Search time 181 Seconds  
(without alignments)  
1799.350 Million cell updates/sec

Title: US-10-088-950A-1  
Perfect score: 3498  
Sequence: 1 MRGGRGAPFLWPLPKALL.....FLTPBELGLGPPRPQVLA 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 O60624	O60624 homo sapien
2	3494	99.9	636	2 O6UWB1	O6UWB1 homo sapien
3	2044	58.4	623	2 O70394	O70394 mus musculus
4	380	10.9	862	1 I12S_HUMAN	O99665 homo sapien
5	329	9.4	861	1 I12S_PIG	O8mj51 sus scrofa
6	328.5	9.4	874	1 I12S_MOUSE	F97378 mus musculus
7	326.5	9.3	861	1 I12S_BOVIN	O9beg2 bos taurus
8	313	8.9	870	2 O6UANO	O6uan0 tetraodon n
9	297.5	8.5	836	1 GCSR_HUMAN	O99062 homo sapien
10	296	8.5	962	2 O65214	O65214 rattus norv
11	292	8.3	971	2 O70458	O70458 mus musculus
12	288.5	8.2	970	2 O88821	O88821 mus musculus
13	277	7.9	837	1 GCSR_MOUSE	P40223 mus musculus
14	250	7.1	918	1 I12S_HUMAN	P40189 homo sapien
15	248	7.1	917	1 I12S_MOUSE	O00560 mus musculus
16	248	7.1	917	2 O6PIT9	O6pdi9 mus musculus
17	244	7.0	813	2 O6DD37	O6dd37 xenopus lae
18	243.5	7.0	813	2 O6UANI	O6uan1 tetraodon n
19	241.5	6.9	918	2 O9WU09	O9w6b1 gallus gall
20	237.5	6.8	881	2 O57519	O57519 xenopus lae
21	229	6.5	710	2 O57520	O57520 xenopus lae
22	226.5	6.5	918	1 I12S_RAT	P40190 rattus norv
23	226	6.5	979	2 O99650	O99650 homo sapien
24	216	6.2	1010	2 O7TQ89	O7tq89 rattus norv
25	212.5	6.1	1083	2 O8QFQ7	O8qfQ7 gallus gall
26	212	6.1	1093	2 O70535	O70535 rattus norv
27	207	5.9	649	2 O6EBC6	O6ebc6 homo sapien
28	207	5.9	662	2 O6EBC3	O6ebc3 homo sapien
29	207	5.9	732	2 O8N117	O8n117 homo sapien
30	207	5.9	764	2 O6EBC4	O6ebc4 homo sapien
31	206.5	5.9	1097	1 LIFR_HUMAN	P42702 homo sapien

32	206	5.9	1092	1 LIFR_MOUSE	P42703 mus musculus
33	193	5.5	582	2 O6UWL8	O6UWL8 homo sapien
34	191	5.5	1304	1 NRCA_HUMAN	O92823 homo sapien
35	185	5.3	844	2 O6UAM8	O6uan8 tetraodon n
36	184.5	5.3	894	2 O6UAM7	O6uan7 tetraodon n
37	182	5.2	716	2 O8RS01	O8rs01 mus musculus
38	181	5.2	716	2 O8K5B1	O8k5b1 mus musculus
39	178.5	5.1	662	2 O6EAL7	O6eal7 mus musculus
40	178	5.1	894	2 O8NSL2	O8ns12 homo sapien
41	174.5	5.0	509	2 O8WYJ0	O8wyj0 homo sapien
42	174	5.0	686	2 O6UAM9	O6uan9 tetraodon n
43	173.5	5.0	1284	2 O6V1767	O6v1767 manduca sex
44	171	4.9	1933	2 O6V3A4	O6v3a4 mus musculus
45	170.5	4.9	547	2 O6EAL6	O6eal6 mus musculus

ALIGNMENTS

RESULT 1  
O60624  
ID O60624 PRELIMINARY; PRT; 636 AA.  
AC O60624;  
DT 01-AUG-1998 (Tremblrel. 07, Created)  
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Class I cytokine receptor (CRL1 protein).  
GN Name=WSX1; Synonyms=CRL1, IL27RA;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98262921; PubMed=9600072; DOI=10.1006/bbrc.1998.8576;  
RA Sprecher C.A., Grant P.J., Baumgartner J.W., Fresnel S.R.,  
RA Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;  
RT "Cloning and characterization of a novel class I cytokine receptor.";  
RL Biochem. Biophys. Res. Commun. 246:82-90 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang W., Wan T., He L., Yuan Z., Cao X.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Maria M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053004; AAC39755.1; -.

submitted  
in IDS

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	9606;
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RRX	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA	Chen J.F., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA	Eaton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heldens S.,
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA	Lewis L., Lisio D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yaneura D.,
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA	Godowski P.;
RT	"The secreted protein discovery initiative (SPDI), a large-scale
RT	effort to identify novel human secreted and transmembrane proteins: a
RT	bioinformatics assessment.";
RL	Genome Res. 13:2265-2270(2003).
EMBL	AY358876; AAQ89235.1; "
DR	InterPro; IPR003961; FN III.
DR	InterPro; IPR008957; FN_III-like.
DR	Pfam; PF00041; Fn3; 2
DR	SMART; SM00060; FN3; 3.
DR	PROSITE; PS50853; FN3; 2.
SQ	SEQUENCE 636 AA; 69459 MW; 473BAAAABD0502B9 CRC64;
	Query Match 99.9%; Score 3494; DB 2; Length 636;
	Best Local Similarity 99.8%; Pred. No. 5.3e-223;
	Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 MRGGGAPFWLWLPKLAALLPLLVLFQTRPGSAGPQCQGVGPLGLDCSWEPGLGL 60
DB	1 MRGGGGFPWLWLPKLAALLPLLVLFQTRPGSAGPQCQGVGPLGLDCSWEPGLGL 60
QY	61 GAPSELHLQSKYSRNTQTVAAGAARSWAIPREQLTMSDKLLVMGTKAGQPLPPVVF 120
DB	61 GAPSELHLQSKYSRNTQTVAAGAARSWAIPREQLTMSDKLLVMGTKAGQPLPPVVF 120
QY	121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPESHKVLICQHYRCCEAAWTLL 180
DB	121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPESHKVLICQHYRCCEAAWTLL 180
QY	181 PELKTIPLTPVEIIODELATGYKVYGRCRMEKEDLNGEWSPILSFQTPPSAKDVMVWG 240
DB	181 PELKTIPLTPVEIIODELATGYKVYGRCRMEKEDLNGEWSPILSFQTPPSAKDVMVWG 240
QY	241 NLCGTGPGEPEPLLWKAPGPCVQVSYPWFVGRELSPEGITCCCSLLPSGAENARVSA 300
DB	241 NLCGTGPGEPEPLLWKAPGPCVQVSYPWFVGRELSPEGITCCCSLLPSGAENARVSA 300
QY	301 VNATSWEPLTNLSVCLDSASAPRSVASSTAGSTELLTWQPGCEPLEHVVDWARDGD 360
DB	301 VNATSWEPLTNLSVCLDSASAPRSVASSTAGSTELLTWQPGCEPLEHVVDWARDGD 360
QY	361 PLEKLNWRLLPPGNLSALLPGNFTVGVPYRITVTVASGLASASSVWGPREELAPLVGP 420
DB	361 PLEKLNWRLLPPGNLSALLPGNFTVGVPYRITVTVASGLASASSVWGPREELAPLVGP 420
QY	421 TLWRLODAPPGETPAIANGEVPRHQIRGHLYTLCAQSGETSPSCVMNSGNTOSTVTLPLD 480
DB	421 TLWRLODAPPGETPAIANGEVPRHQIRGHLYTLCAQSGETSPSCVMNSGNTOSTVTLPLD 480
QY	481 PNGPCELWTVASTIAGQGPPGPIRLRLHLPDNTLRWKVLPGLFLWGLFLIGCGLSLATSG 540
DB	481 PNGPCELWTVASTIAGQGPPGPIRLRLHLPDNTLRWKVLPGLFLWGLFLIGCGLSLATSG 540
QY	541 RCYHLRHKLPRWWVKVDPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPPPWNSS 600
DB	541 RCYHLRHKLPRWWVKVDPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPPPWNSS 600
QY	601 QPAQATAPLDSGYEKHFLLPTPEELGILLGPPRPQVLA 636

601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

|||||

# RESULT 3

O70394  
ID 070394 PRELIMINARY; PRT; 623 AA.  
AC O70394  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Class I cytokine receptor (Interleukin 27 receptor, alpha).  
GN Name=IL27ra; Synonyms=Wx1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98262921; PubMed=9600072; DOI=10.1006/bbrc.1998.8576;  
RA Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,  
RA Schrader S.K., Yamaguchi T., Whitmore T.E., O'Hara P.J., Foster D.F.;  
RT "Cloning and characterization of a novel class I cytokine receptor.";  
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heish F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedon T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rounfard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AF053005; AAC40121.1; -.  
DR ENBL; BC032878; AAH32878.1; -.  
DR HSSP; P05710; 1F6P.  
DR MGD; MGI:1355318; I127ra.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0042607; F:exogenous peptide antigen binding; IDA.  
DR GO; GO:0045509; F:interleukin-27 receptor activity; IDA.  
DR GO; GO:0042287; F:MHC protein binding; IDA.  
DR GO; GO:0005515; P:immune response; TAS.  
DR GO; GO:0006955; P:protein binding; IPI.  
DR InterPro; IPR003961; FN III.  
DR Pfam; PF00041; fn3; 1.  
DR PROSITE; PS00853; FN3; 2.  
KW Receptor.  
SQ SEQUENCE 623 AA; 68998 MW; 4BA20FEC875A7180 CRC64;

Query Match 58.4%; Score 2044; DB 2; Length 623;  
Best Local Similarity 62.8%; Pred. No. 5.2e-127;  
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY 14 LPKALLPLLMVLVFORTRPGQSAGPLQCYGVGPGDLNCSWEPGLDGPSEHLQSQKY 73  
DB 9 LTPLELLLSLMSLLGTRPHGSPGLQCYSGVPLGILNCSWEPGLDLETPELVYHQSKY 68  
QY 74 RSNKTQTVAAAGRSWAIPREQLTMSDKLLVNGTKAGQPLWPPVFNLTQMKPNAPRL 133  
DB 69 HPNRVMEVKPSKOSWVITPREQFTWADKLLIWTQKGRPLMSVSVNLTQMKPDTPQI 128  
QY 134 GPQVDFSEDDPLEATVHAPPTWPSHKVLICQHYRRQCEAAWTLPELTKTTPLEVEI 193  
DB 129 FSQVDISEATLEATVQWAPPVPPQKALTQRYKECOAEWTRLEPQKTDGLTPVEM 188  
QY 194 QDLELATGYKYGRCKMEKEEDLWGSWSPILSFQTPPSAPKVVVSGNLCTPGCEPLL 253  
DB 189 QNLEPGTCYQSGRCQVENGYP-WGEWSSPLSFQTPFLDPEDVWVSGTCVETSCKRAALL 247  
QY 254 LMKAPGPCQVSYKVMFWVGRRLSPGEGITCCCLIPSGAEWARSVAVNATSWPLTNLS 313  
DB 248 VKDPRPCQVTVTVWFGAGDITTTQEEVPCCKSPVPMWENAVVSGNSTSWVPPTNLS 307  
QY 314 LVCLDSASAPRSVAVSSIAGSTELLVTWQPGCEPLEHVVDWARDGDPLEKLNKVRLLPPG 373  
DB 308 LVCLAPESAPCDVGSVSADGSPGKIVTKQGTREPLEYVVDNAQDGDSDLNWTNRLPPG 367  
QY 374 NLSALLPGNFTVGVYRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPGTP 433  
DB 368 NLSTLLPGFKGVPYRITVTAVYSGLAAPSVWGFREELVPLAGVAVWRLPDDPGTP 427  
QY 434 AIWGEVPRHOLRGHLTHYTLCAQSGTSPVCMVSGNTQSVTLDPDPWGCBLWWTAST 493  
DB 428 VWAMGEVPRHOLRGHATHTYTCQSRGLSTVCRVSSQTQTATPLNLHSGSFKLWTVST 487  
QY 494 IAQCGPPGPTLRLLHLPDNTLRWVKVLCILFLWGLFLGLGCLSLATS---GRCVHLRHKV 549  
DB 488 VACQGGPPGDLSTLHLPDNRIRKALPWFSLWGLLGLGCLSLATSRLCQARCLWHRKL 547  
QY 550 LPRWVWEKVPDPANSSSGOPHMEQVPEAQLGLDPLILEVEEMPPPPVMESSQAQAPL 609  
DB 548 LPQWIERVDPDPANSSSGOPYKEVSLPQPKDGPILVEVEELQPVVES--PKASAPI 604  
QY 610 DSGYKHFLLTPPELGLL 627  
DB 605 YSGYKHFLLTPPELGLL 622

## RESULT 4

ID 112S\_HUMAN STANDARD; PRT; 862 AA.  
AC Q99665;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2)  
DE (IL-12R-beta2).  
GN Name=IL12RB2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97098510; PubMed=8943050; DOI=10.1073/pnas.93.24.14002;  
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,  
RA Gately M.K., Gubler U.;  
RT "A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=T-cell;  
RX PubMed=10663559;  
RA van Rietschoten J.G.I., Smits H.H., Westland R., Verweij C.L.,

den Hartog M.T., Wierenga E.A.;  
"Genomic organization of the human interleukin-12 receptor beta2-chain  
gene."; Immunogenetics 51:30-36(2000).  
[3]  
RL INTERACTION WITH STAT4, AND MUTAGENESIS OF LEU-801; PRO-802; SER-803  
RP AND ASN-804.  
RX PubMed=10415122; DOI=10.1006/abbi.1999.1302;  
RA Yao B.B., Niu P., Surowy C.S., Faltynek C.R.;  
"Direct interaction of STAT4 with the IL-12 receptor."; Arch.  
RL Biochem. Biophys. 368:147-155(1999).  
[4]  
RN INTERACTION WITH JAK2, AND MUTAGENESIS OF TYR-678; TYR-767 AND  
RP TYR-800.  
RX PubMed=10198225; DOI=10.1006/bbrc.1999.0479;  
RA Yamamoto K., Shibata F., Miura O., Kamiyama R., Hirose S.,  
RA Miyasaka N.;  
"Physical interaction between interleukin-12 receptor beta 2 subunit  
and Jak2 tyrosine kinase: Jak2 associates with cytoplasmic membrane-  
proximal region of interleukin-12 receptor beta 2 via amino-  
terminus."; J. Biol. Chem. 274:11875-11878(1999).  
[5]  
RL Biochem. Biophys. Res. Commun. 257:400-404(1999).  
RN INTERACTION WITH STAT4, AND MUTAGENESIS OF TYR-678; TYR-767 AND  
RP TYR-800.  
RX PubMed=9890938; DOI=10.1074/jbc.274.4.1875;  
RA Naeger L.K., McKinney J., Salvekar A., Hoey T.;  
"Identification of a STAT4 binding site in the interleukin-12 receptor  
required for signaling."; J. Exp. Med. 185:825-831(1997).  
[6]  
RN TISSUE SPECIFICITY, AND INDUCTION.  
RX PubMed=9120388;  
RA Rogge L., Barberis-Maino L., Biffi M., Passini N., Presky D.H.,  
RA Gubler U., Sinigaglia F.;  
"Selective expression of an interleukin-12 receptor component by human  
T helper 1 cells."; J. Exp. Med. 185:825-831(1997).  
[7]  
RN PHOSPHORYLATION, INTERACTION WITH SOCS3, AND MUTAGENESIS OF TYR-678;  
RP TYR-767 AND TYR-800.  
RX PubMed=14559241; DOI=10.1016/j.bbrc.2003.09.140;  
RA Yamamoto K., Yamaguchi M., Miyasaka N., Miura O.;  
"SOCS-3 inhibits IL-12-induced STAT4 activation by binding through its  
SH2 domain to the STAT4 docking site in the IL-12 receptor beta2  
subunit."; Biochem. Biophys. Res. Commun. 310:1188-1193(2003).  
[8]  
RN VARIANTS GLY-313 AND ARG-720.  
RX PubMed=10600539; DOI=10.1006/bbrc.1999.1859;  
RA Matsui E., Kaneko H., Fukao T., Teramoto T., Inoue R., Watanabe M.,  
RA Kasahara K., Kondo N.;  
"Mutations of the IL-12 receptor beta2 chain gene in atopic  
subjects."; Biochem. Biophys. Res. Commun. 266:551-555(1999).  
RL Biochem. Biophys. Res. Commun. 266:551-555(1999).  
CC -1- FUNCTION: Receptor for IL-12. This subunit is the signaling  
component coupling to the JAK2/STAT4 pathway. Promotes the  
proliferation of T-cells as well as NK cells. Induces the  
promotion of T-cells towards the Th1 phenotype by strongly  
enhancing IFN-gamma production.  
CC -1- SUBUNIT: Heterodimer/heterotrimer; disulfide-linked. The  
functional high affinity IL12 receptor is composed of IL12RB1 and  
IL12RB2. IL12RB2 binds JAK2 (via its N-terminal) through a  
membrane-proximal region of the cytoplasmic domain. Interaction,  
in vitro and in vivo, with SOCS3 (via its SH2 domain) inhibits the  
STAT4-mediated activation. Binds STAT4 through a membrane-distal  
C-terminal region.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1;  
Isoid=Q99665-1; Sequence=Displayed;  
Name=2;

Isoid=Q99665-2; Sequence=VSP\_011112, VSP\_011113;  
TISSUE SPECIFICITY: Isoform 2 is expressed at similar levels in  
both naive and activated T-cells.  
-1- DEVELOPMENTAL STAGE: Maximum levels in Th1 cells between day 3 and  
day 8 of activation.  
-1- INDUCTION: In vitro, up-regulated by interferon alpha.  
-1- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
folding and thereby efficient intracellular transport and cell-  
surface receptor binding.  
-1- DOMAIN: The box 1 motif is required for JAK interaction and/or  
activation.  
-1- PTM: On IL12 binding, phosphorylated on C-terminal tyrosine  
residues by JAK2. Phosphorylation on Tyr-800 is required for STAT4  
binding and activation, and for SOCS3 binding.  
-1- POLYMORPHISM: Heterozygotic variants Gly-313 and Arg-720 are  
associated with atopy, an immunological condition that can lead to  
clinical symptoms such as allergic rhinitis, sinusitis, asthma and  
eczema.  
-1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
-1- SUBFAMILY 2: Contains 5 fibronectin type III domains.  
-1- SIMILARITY: Contains 5 fibronectin type III domains.  
-----  
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or send an email to license@isb-sib.ch).  
-----  
EMBL; U64198; AAB36675.1; -  
HSSP; P05710; 1P6F.  
Genew; HGNC:5972; IL12RB2.  
MIM; 601642; C: integral to plasma membrane; TAS.  
GO; GO:0005887; C: integral to plasma membrane; TAS.  
GO; GO:0004907; F: interleukin receptor activity; TAS.  
GO; GO:0007166; P: cell surface receptor linked signal transdu. ; TAS.  
GO; GO:0008284; P: positive regulation of cell proliferation; TAS.  
InterPro; IPR002996; Cytokn recept\_B/G.  
InterPro; IPR003961; FN\_III.  
InterPro; IPR008957; FN\_III-like.  
InterPro; IPR003529; Hemtrecept\_1302.  
InterPro; IPR010457; Lep\_receptor\_19.  
Pfam; PF00041; fn3; 3.  
Pfam; PF06328; Lep\_receptor\_Ig; 1.  
PROSITE; PS00853; FN3; 5.  
PROSITE; PS01353; HEMATOPO REC L F2; 1.  
Alternative splicing; Glycoprotein; Phosphorylation; Polymorphism;  
Receptor; Repeat; Signal; Transmembrane.  
KW SIGNAL 1 23  
Potential.  
FT CHAIN 24 862 Interleukin-12 receptor beta-2 chain.  
FT DOMAIN 24 622 Extracellular (potential).  
FT TRANSMEM 623 643 Potential.  
FT DOMAIN 644 862 Cytoplasmic (potential).  
FT DOMAIN 124 218 Fibronectin type-III 1.  
FT DOMAIN 224 316 Fibronectin type-III 2.  
FT DOMAIN 317 415 Fibronectin type-III 3.  
FT DOMAIN 420 517 Fibronectin type-III 4.  
FT DOMAIN 521 617 Fibronectin type-III 5.  
FT DOMAIN 208 211 Poly-Ser.  
FT DOMAIN 750 753 Poly-Pro.  
FT SITE 305 309 WSXWS motif.  
FT SITE 662 670 Box 1 motif.  
FT SITE 796 801 Required for STAT4 binding.  
FT MOD\_RES 800 800 Phosphotyrosine.  
FT CARBOHYD 48 48 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 129 129 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 166 166 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 195 195 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 271 271 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 347 347 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 376 376 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 480 480 N-linked (GlcNAc...) (potential).

FT VARSPLIC 650 659 VFVLLAALRP -> RHSCPWTGS (in isoform 2).  
FT VARSPLIC 660 862 Missing (in isoform 2).  
FT VARSPLIC 660 862 /FTid=VSP\_011112.  
FT VARIANT 185 185 I -> V (in dbSNP:2307146).  
FT VARIANT 201 201 /FTid=VAR\_014805.  
FT VARIANT 201 201 T -> I (in dbSNP:7526769).  
FT VARIANT 313 313 /FTid=VAR\_019525.  
FT VARIANT 313 313 R -> G.  
FT VARIANT 420 420 /FTid=VAR\_019526.  
FT VARIANT 420 420 G -> R (in dbSNP:2307148).  
FT VARIANT 426 426 /FTid=VAR\_014806.  
FT VARIANT 426 426 Q -> H (in dbSNP:2307145).  
FT VARIANT 465 465 /FTid=VAR\_014807.  
FT VARIANT 465 465 G -> D (in dbSNP:2307153).  
FT VARIANT 625 625 /FTid=VAR\_014808.  
FT VARIANT 625 625 A -> V (in dbSNP:2307154).  
FT VARIANT 720 720 /FTid=VAR\_016097.  
FT VARIANT 720 720 H -> R.  
FT MUTAGEN 678 678 /FTid=VAR\_019527.  
FT MUTAGEN 678 678 Y->F: No loss of STAT4 activation. No  
FT MUTAGEN 767 767 loss of SOCS3 binding.  
FT MUTAGEN 767 767 Y->R: No loss of STAT4 activation. No  
FT MUTAGEN 800 800 loss of SOCS3 binding.  
FT MUTAGEN 800 800 Y->E: Loss of STAT4 activation. Abolishes  
FT MUTAGEN 801 801 SOCS3 binding.  
FT MUTAGEN 801 801 L->A: Abolishes in vitro STAT4 binding to  
FT MUTAGEN 802 802 a phosphorylated Y-800 peptide.  
FT MUTAGEN 802 802 P->A: No effect on in vitro STAT4 binding

Query Match 10.9%; Score 380; DB 1; Length 862;  
Best local similarity 25.3%; Pred. No. 1,1e-16;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPLOCYGVPLGDLNCSWEPLGD-----LCAPSELHLSQ----- 71  
DB 126 QPON-----LSCIQKGEGTACTWGERDTHLYTEYTLQSGPKNLTWQCKDIYCDYL 181  
QY 72 -----KYRSMKTTQV-AVAGRSWVAIPREQLTMSDKLWGTGKAGQPLMPVFN 121  
DB 182 DFGINLTPESPENFTAKVTAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231  
QY 122 LETQMKPNARLPGDVFSDDEPLEATVHWAPPFWPSHKVLIQFHYRRCOEAAWTLLEP 181  
DB 232 IKFQ-KASVSR-----CTLYNR-----DEGLVLLNRLRYRPSNRLNWN--- 269  
QY 182 ELKTIPLTPV-----EIODELATCYKYVGRCKMEKEEDLWGESPILSFOTP---SPAPX 234  
DB 270 -----VNVTKAKGRHDLDLKPFTEYEFQISKLHLXKGSWSDWSESRLAQTPPEEPTGML 325  
QY 235 DVVSGNLCTPGGEEPELLWK-----APGPCVQVSKYKWFVWVGRELSPG--GITCCC 286  
DB 326 DVWYMKRHIDY-SRQQLSLFWKLSVSEARGKILHVQVTLQELTGKAMQNTIGHTSWT 384  
QY 287 SLIPSGAWEA-RVSAVNA--TSWEPLNLVLCLDSASAPRSVAVSSIAGSTELLVTWQP 343  
DB 385 TVIPRTGNWAVAVSAANSKSSLPTRINIMLCEAGLLAPROVSANS-EGMDNLTWQP 443  
QY 344 ---GPGEPLHVDWAR---DGDPLEKLNVRPLPGNLSALLPGNFVGVPIYITVAVS 397  
DB 444 PRKDPASQVQVYVWEWRELHPGGDTQVPLNLRSPYNVSAISGNTKSYICYRIVYALS 503  
QY 398 ASGLASASSVWGPREELAPLVGPTLWRLQDAPCTPAIANGVEPRHQLRGLHLYTLIC-- 455  
DB 504 GD-QGGCSSILGSKKHAPLSGPHNAITB-EKGSILISWNSIPVQBMGCLLHYRIYWK 561  
QY 456 -AQSGETSPSVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQGPPIRLHLHPDN 511  
DB 562 ERDSNSQQLCEIPYRVSONSHPLNSLQ-PRVTVLWMTALTAAAGSSHGNEREFCL-QG 619  
QY 512 TLRWK--VLPGI----LFLWGLFLLCGGLSLATSGRCVHLRHKL-----PRWWEKVP 559  
DB 620 KANWMAFVAPSICIAIIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667

QY 560 DPANSSSGQPH-----MEQVPEAQPLGDLPILEVEEMEPVPPVMESSQPAQATA-----PLD 610  
DB 668 DPANSTCAKYPFAAEKTKQLPLDLRLIDWPTP-----DPEPLVISEVLHVQVTPVFRHPPC 723  
QY 611 SGYEKHLFLTPBELGLLG-----PPRQVLT 635  
DB 724 SNWPQ-----REKGIQGHQASEKMMHSSASSPPPPRAL 756

RESULT 5  
IL2S\_PIG STANDARD; PRT; 861 AA.  
AC Q8MJ51; Q8WN24;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 beta2 receptor)  
DE (IL-12RBeta2).  
GN Name=IL12RB2;  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Periphereal blood monocytes;  
RX PubMed=12543551; DOI=10.1016/S0165-2427(02)00288-X;  
RA Kokubo T., Inumaru S., Watanabe S., Kubota T.,  
RT "Cloning of porcine interleukin (IL)-12 receptor beta2 (IL-12beta2)  
RT gene and its application to a rapid biological assay for human/porcine  
RT IL-12.";  
RL Vet. Immunol. Immunopathol. 91:155-160(2003).  
RN [2]  
RP SEQUENCE OF 12-859 FROM N.A.  
RC TISSUE=Lymphoblast;  
RX PubMed=12383645; DOI=10.1016/S0165-2427(02)00205-2;  
RA Solano-Aguilar G.I., Zarlenga D., Beshah E., Vengroski K.,  
RA Gasbarre L., Junker D.E., Cochran M.D., Weston C.O., Valencia D.M.,  
RA Chiang C., Dawson H.D., Urban J.F. Jr., Lunney J.K.;  
RT "Limited effect of recombinant porcine interleukin-12 on porcine  
RT lymphocytes due to a low level of IL-12 beta2 receptor.";  
RL Vet. Immunol. Immunopathol. 89:133-148(2002).  
RN [3]  
RP ERRATUM.  
RA Solano-Aguilar G.I., Zarlenga D., Beshah E., Vengroski K.,  
RA Gasbarre L., Junker D.E., Cochran M.D., Weston C.O., Valencia D.M.,  
RA Chiang C., Dawson H.D., Urban J.F. Jr., Lunney J.K.;  
RL Vet. Immunol. Immunopathol. 95:183-183(2003).  
CC -I- FUNCTION: Receptor for IL-12. This subunit is the signaling  
CC component coupling to the JAK2/STAT4 pathway.  
CC -I- SUBUNIT: Heterodimer/heteroligomer; disulfide-linked. The  
CC functional high affinity IL12 receptor is composed of IL12RB1 and  
CC IL12RB2. IL12RB2 binds JAK2 (via its N-terminal) through a  
CC membrane-proximal region of the cytoplasmic domain (By  
CC similarity).  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- DOMAIN: The WXXXX motif appears to be necessary for proper protein  
CC folding and thereby efficient intracellular transport and cell-  
CC surface receptor binding.  
CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or  
CC activation.  
CC -I- PTM: On IL12 stimulation, phosphorylated on C-terminal tyrosine  
CC residues (By similarity).  
CC -I- SIMILARITY: Belongs to the type I cytokine family of receptors.  
CC Subfamily 2.  
CC -I- SIMILARITY: Contains 5 fibronectin type III domains.  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF330213; AAM47543.1; -

CC EMBL; AF448143; AAL60218.1; -

CC HSSP; P40189; 1BOU

DR InterPro; IPR002996; Cytn\_recept\_B/G.

DR InterPro; IPR010457; Lep\_receptor\_19.

DR Pfam; PF06328; Lep\_receptor\_19.

DR Pfam; PF06328; Lep\_receptor\_19.

DR SMART; SM00060; FN3; 4.

DR PROSITE; PS00853; FN3; 5.

DR PROSITE; PS01353; HEMATOPO\_REC\_L\_P2; 1.

DR Glycoprotein; Receptor; Repeat; Signal;

KW Transmembrane.

FT SIGNAL 1 23 Potential.

FT CHAIN 24 861 Interleukin-12 receptor beta-2 chain.

FT DOMAIN 24 622 Extracellular (Potential).

FT TRANSMEM 623 643 Potential.

FT DOMAIN 644 861 Cytoplasmic (Potential).

FT DOMAIN 124 218 Fibronectin type-III 1.

FT DOMAIN 224 316 Fibronectin type-III 2.

FT DOMAIN 317 415 Fibronectin type-III 3.

FT DOMAIN 420 518 Fibronectin type-III 4.

FT DOMAIN 521 616 Fibronectin type-III 5.

FT DOMAIN 750 753 Poly-Pro.

FT SITE 305 309 WSXWS motif.

FT SITE 662 670 Box 1 motif.

FT CARBOHYD 48 48 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 129 129 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 166 166 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 271 271 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 376 376 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 480 480 N-linked (GlcNAc. . .) (Potential).

FT CONFLICT 212 214 LPS -> FPC (in Ref. 2).

FT CONFLICT 218 218 F -> L (in Ref. 2).

FT CONFLICT 239 239 V -> M (in Ref. 2).

FT CONFLICT 404 404 G -> S (in Ref. 2).

FT CONFLICT 474 474 L -> P (in Ref. 2).

FT CONFLICT 509 509 C -> R (in Ref. 2).

FT CONFLICT 736 736 R -> H (in Ref. 2).

FT CONFLICT 805 805 M -> I (in Ref. 2).

FT CONFLICT 848 848 A -> T (in Ref. 2).

FT SEQUENCE 861 AA; 96055 MW; 2AB663E3C5F42534 CRC64;

Query Match 9.4%; Score 329; DB 1; Length 861;

Best Local Similarity 25.0%; Pred. No. 2.6e-13;

Matches 164; Conservative 82; Mismatches 264; Indels 146; Gaps 36;

QY 31 RPOGAGPLOCYGVPLGDLNCSWEPLGD-----LGAPSELHLSQ--KYRSNKT 78

DB 126 QPQN-----VSCMKGERTVACSWDRGRDTHLYTATLQNGPKNTWQKQSDYVCDLSL 181

QY 79 QTVAAGRSWVAIPRE-----QUTMSDKLLVMGTAKAGPLWPPVFNLETOMKPN 130

DB 182 DL-----GINLPSPSSSYTAQVTAIINSL---GTASS---LPSFTFLDV-VRPLP 226

QY 131 PRLGPDVDFEDDDPLEATVHAPPTWPSH-KVLICQHYRRCQEAATWLEPLKTIPLT 189

DB 227 PW-----DIRIK---CVNASVSTCTLQWRDEGLVLLNRLRYPVYSRSMNMYN---ATNAKG 277

QY 190 PVEIQDLLELATGVYKRCMEKEEDLWGEWSPILSFQTP---PSAPKDVWVSNLCGTP 246

DB 278 RHDVLDLKPFTFEYFQISKPHLOKGRWSWSLSRTQTPEKPTGMLDVWYMKQHIDYK 337

QY 247 GGEPLLLWK-----APGPCVQVSYKV-----WVVGRELSP 280

DB 338 -RQISLFWKNLSSEARGKILH--YQVTLQEAAGNATLQNIERNSTWT----- 386

QY 281 GITCCSLIPGSAFW-ARVSANVA--TSWEPLTNLSLVCLDSASAPSVASSIAGSTEL 337

DB 387 -----IPTGIWAASAAANSKGSLSLPTRIINADLCGALLAPQOVSANP-EGSDNL 437

QY 338 LVTV--QPGCEPL--EHVVDWAR---DGDPLEKLNWRLPPGNLSALLPGNFTGVGPYRI 391

DB 438 LVKWTSPCEGATAVQEVVREHLHGGNQPLSLWLRSPYNTSTLISDNKIPYICYEI 497

QY 392 TVTAVSAGSLASASSVWGFEEELAPLVGPTLMRLQDAPCTPAIANGVEPRHQLRGLTH 451

DB 498 RVHALSGD-QGGCSSIRGDLKHKAPLSGPHINAISE-EKGSILISWDEIPAQOMGCILH 555

QY 452 YTLC---AQSGTSPSYC---MNVSGNTQSVTLFDLPWGPCELWVTASTIAGQGPPIILR 505

DB 556 YRIYWKERDSQPCICEIPYRSPKSHPIINSLQ-PRVTYVLMWTALTATAGESPQGNERE 614

QY 506 LHLPDNLTNRWK--VLPGL---LFLWGLFLGLGCLSLATSGRCYHLRHKVL-----PRVW 555

DB 615 FCL-QGKANWSTFVAPSICTAVITGVVF-----SMRCFRQKVFVLLALRPQWCS 663

QY 556 EKVPDPANSSGQPH-----MEQVPEAQPLGDLPILEVEEMEPVWESSQPAQAT 606

DB 664 REIPDPANSTWAKYPIVEEKKQLSLDRLLADWPTPE---EPEPLVINEVLPQVT 715

RESULT 6

112S MOUSE

ID 112S MOUSE STANDARD; PRT; 874 AA.

AC P97378;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 25-OCT-2004 (Rel. 45, Last annotation update)

DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).

GN Name=112rb2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97098510; PubMed=8943050; DOI=10.1073/pnas.93.24.14002;

RA Preeky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y., Gately M.K., Gubler U.

RT "A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits."

RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).

RN [2]

RP FUNCTION IN STAT3/STAT4 ACTIVATION, AND MUTAGENESIS OF TYR-677;

RX TYR-693; TYR-727; TYR-737; TYR-748; TYR-757; TYR-778; TYR-804; TYR-811 AND TYR-866.

RX PubMed=12370372;

RA Nishikomori R., Usui T., Wu C.-Y., Morinobu A., O'Shea J.J., Strober W.

RT "Activated STAT4 has an essential role in Th1 differentiation and proliferation that is independent of its role in the maintenance of IL-12R beta 2 chain expression and signaling."

RL J. Immunol. 169:4388-4398(2002).

RN [3]

RP DEVELOPMENTAL STAGES.

RX PubMed=9120387;

RA Szabo S.J., Dighe A.S., Gubler U., Murphy K.M.;

RT "Regulation of the interleukin (IL)-12R beta 2 subunit expression in developing T helper 1 (Th1) and Th2 cells."

RL J. Exp. Med. 185:817-824(1997).

RN [4]

RP IL12 UNRESPONSIVENESS IN CR MUTANT MICE.

RX PubMed=11489994;

RA Poltorak A., Meriin T., Nielsen P.J., Sandra O., Smirnova I., Schupp I., Boehm T., Galanos C., Freudenberg M.A.;

RT "A point mutation in the IL-12R beta 2 gene underlies the IL-12 unresponsiveness of lps-defective C57BL/10ScCr mice."

RL J. Immunol. 167:2106-2111(2001).

CC -!- FUNCTION: Receptor for IL-12. This subunit is the signaling component coupling to the JAK2/STAT4 pathway. Promotes the proliferation of T-cells as well as NK cells. Induces the



CC promotion of T-cells towards the Th1 phenotype by strongly  
CC enhancing IFN-gamma production. Can also activate STAT3.  
CC -1- SUBUNIT: Heterodimer/heterotrimer; disulfide-linked. The  
CC functional high affinity IL12 receptor is composed of IL12RB1 and  
CC IL12RB2. IL12RB2 binds JAK2 (via its N-terminal) through a  
CC membrane-proximal region of the cytoplasmic domain (5b  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in developing T helper (TH) cells.  
CC -1- DEVELOPMENTAL STAGE: Expressed at high levels in Th1 cells on day  
CC 3, 5 and 7 after primary activation. Very low expression in Th2  
CC cells on day 3 and not detectable on day 5 nor day 7 after  
CC activation.  
CC -1- INDUCTION: Following T cell activation, expression inhibited by  
CC IL4 and induced by IFN gamma.  
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
CC folding and thereby efficient intracellular transport and cell-  
CC surface receptor binding.  
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or  
CC activation.  
CC -1- PTM: On IL12 stimulation, phosphorylated on C-terminal tyrosine  
CC residues. Phosphorylation of any one of Tyr-757, Tyr-804 or Tyr-  
CC 811 can activate STAT4, IFN-gamma production, and T-cell  
CC proliferation. Tyr-811 is the dominant site of cell proliferation.  
CC -1- MISCELLANEOUS: Lps-defective mice C57BL/10ScCr (Cr) mice carry a  
CC mutation in the IL12RB2 gene leading to the production of a  
CC truncated IL12 receptor beta 2 chain resulting in malfunction of  
CC the IL12-mediated IFN-gamma response.  
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
CC Subfamily 2.  
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC ENMBL; U64199; AAB36676.1; ..  
CC MGD; MGI:1270861; IL12RB2.  
CC InterPro; IPR002996; Cytok\_recept\_B/g.  
CC InterPro; IPR003961; FN III.  
CC InterPro; IPR008957; FN III-like.  
CC InterPro; IPR003529; Hemtrecept\_1302.  
CC InterPro; IPR010457; Lep\_receptor\_Ig.  
CC Pfam; PF00041; fn3; 4.  
CC Pfam; PF06328; Lep\_receptor\_Ig; 1.  
CC PROSITE; PS50853; FN3; 5.  
CC PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
CC Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 23 Potential.  
FT CHAIN 24 874 Interleukin-12 receptor beta-2 chain.  
FT DOMAIN 24 637 Extracellular (Potential).  
FT TRANSMEM 638 658 Potential.  
FT DOMAIN 659 874 Cytoplasmic (Potential).  
FT DOMAIN 137 234 Fibronectin type-III 1.  
FT DOMAIN 240 332 Fibronectin type-III 2.  
FT DOMAIN 334 430 Fibronectin type-III 3.  
FT DOMAIN 435 532 Fibronectin type-III 4.  
FT DOMAIN 533 631 Fibronectin type-III 5.  
FT SITE 321 325 WSXWS motif.  
FT SITE 677 685 Box 1 motif.  
FT MOD\_RES 757 757 Phosphotyrosine (Probable).  
FT MOD\_RES 804 804 Phosphotyrosine (Probable).  
FT MOD\_RES 811 811 Phosphotyrosine (Probable).  
FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 224 224 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 279 279 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 323 323 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).  
FT MUTAGEN 677 677 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 693 693 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 727 727 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 737 737 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 748 748 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 757 757 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 778 778 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 804 804 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 811 811 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
FT MUTAGEN 866 866 Y->F: No loss of IL12-induced STAT4  
FT activation nor T-cell proliferation. No  
FT effect on IFN-gamma production.  
SQ SEQUENCE 874 AA; 98196 MW; 5825421BFI6D67 CRC64;  
Query Match 9.4%; Score 328.5; DB 1; Length 874;  
Best Local Similarity 23.0%; Pred. No. 2.9e-13;  
Matches 153; Conservative 91; Mismatches 268; Indels 153; Gaps 32;  
Qy 39 LQCYGVPLGLDNCSEPP-----LGDGAPSELHLQSKYRSNKTQ----- 79  
Db 143 ISCVQEGENGTVACSWNSGKVTYLTNTYTLQLSGPNNLTCCQCFSDNRQNCNRLDLGIN 202  
Qy 80 -TVAAAGRSWVAIPR-EQLTMSDKLLVMGTAGQPLWPPVFVNLETQMKPNAPRLGPDV 137  
Db 203 LSPDLAESRIVRVTAINDLGNSSSL-----PHTFTFLDIVIP--LPPWDIRI 248  
Qy 138 DFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLPELKTIPLTVPVEIODLE 197  
Db 249 NFLNASSRGCTLQWE---DEGOVLNQLRYQPLNSTSNMNVN---ATNAKGKVDLRDLR 301  
Qy 198 LATGYKYGRCKMEKEEDLWGEWSPILSPOTPSAP---KDVN-----VSGNL 242  
Db 302 PFTFEBFQISKLHLGGGWSNWSNSESRLTRTPPEEPVGLDILWYMKQDIDYDROQIS--- 358  
Qy 243 CGTPGGEPEPLLWKAQPCQVQSVKWFVWVGRELSPGEGI-----TCCCSLIPSGAEW 295  
Db 359 -----LFWKSLNPSSEARGLIHYQVTLQEVTKTKTLQNTTRHTSWTRVIFRTGAW 408  
Qy 296 -ARVSVAATSWEPNLNLSIV--CLDSASAPRSVAVSSISTAGSTELLVWTFP---GPGEPL 349  
Db 409 TASVSAANSKASAPTHINIVDLCTGTLGLAPHQVSAS-ENMDNILLVWTPPKKADSAVR 467  
Qy 350 EHVVDW-ARDGDPLEKL--NWRLPPEGNLSALLPGNFTVGVPYRITVTVASGLASAS 406  
Db 468 EYVWRAQLQGSITKTFPPHWRIRIPDNNMSALISENIKPYICVEIRVHALSES-QGCGSS 526

DR	EMBL; AJ308426; CAC28320.1; -.
DR	HSP; P40189; 1BQU.
DR	GO; GO:0042022; C:interleukin-12 receptor complex; NAS.
DR	GO; GO:0016517; F:interleukin-12 receptor activity; NAS.
DR	InterPro; IPR002996; Cytn recept_B/G.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR003529; Hemprrecept_L302.
DR	InterPro; IPR010457; Lep_receptor_Ig.
DR	Pfam; PF00041; fn3; 3.
DR	Pfam; PF06328; Lep_receptor_Ig; 1.
DR	SMART; SM00060; FN3; 4.
DR	PROSITE; PS00853; FN3; 5.
DR	PROSITE; PS01353; HEMATOPO REC_L_F2; 1.
KW	Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
KW	Transmembrane.
FT	SIGNAL 1 23 Potential.
FT	CHAIN 24 861 Interleukin-12 receptor beta-2 chain.
FT	DOMAIN 24 622 Extracellular (Potential).
FT	TRANSMEM 623 643 Potential.
FT	DOMAIN 644 861 Cytoplasmic (Potential).
FT	DOMAIN 124 218 Fibronectin type-III 1.
FT	DOMAIN 224 316 Fibronectin type-III 2.
FT	DOMAIN 317 415 Fibronectin type-III 3.
FT	DOMAIN 420 518 Fibronectin type-III 4.
FT	DOMAIN 521 616 Fibronectin type-III 5.
FT	DOMAIN 750 753 Poly-Pro.
FT	SITE 305 309 WSXWS motif.
FT	SITE 662 670 Box 1 motif.
FT	SITE 800 806 Required for STAT4 binding (By similarity).
FT	CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 271 271 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).
SEQ	SEQUENCE 861 AA; 96208 MW; 487B1E5D1E358E5B CRC64;
Query Match 9.3%; Score 326.5; DB 1; Length 861;	
Best Local Similarity 24.5%; Pred. No. 3.8e-13;	
Matches 171; Conservative 88; Mismatches 281; Indels 157; Gaps 36;	
Qy	39 LQCVGVCPLGDNLCSWEPLGD-----LGAPSELHLQSQ----- 71
Dd	130 LSCIQKRGRTVCTWIRGRDTHLYATYLAQNGPKLTWKQCNHDYCDHLDLGINLTP 189
Qy	72 -KYRSNKT-QTVAAAGRSWVAIPREQLTMSDKLLVMGTGAKGPLMPPVFVNLTOMKPN 129
Dd	190 ESLESSYTKVTAINSLGSASSP-PFSTLLDIV-----RPL-PFWDIRIKF----- 234
Qy	130 APRLGPDVDSDDPLEATVHWAPPTWPSHKVLICQFYHRCEQAATWLLELPKTIPLT 189
Dd	235 -----VNASVD---RCTLLWR---DEGLVLRLRYRPINRSRWNVN---VTNAGK 277
Qy	190 PVEIQDLRELATGYKVYCKRMKEEDLWGEWSPILSFQTPEPSAP---KDWM-----VSGN 241
Dd	278 RHDLLDLKPFEYEFQISKKLHYKGSDWSLSRTQTPPEEPIGMLNVMYMRQHIDYN 337
Qy	242 LCGTFGEEEPDLLWK-----APGCQVOVSYYKWFW-VGBELSFEGITCCCS---LIIPS 291
Dd	338 -----RQIISLFKNLSSLSEARGKILH--YQVTLQKVAGEITLQNI TEHTSWTWVIPR 389
Qy	292 GAEW-ARVASNA--TSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWOP---GP 345
Dd	390 TGNWAAAVSAANSKSSLPTRINTIDLCGAELLAPQQVLAKS--EGMDKLMTWTTPPEKAT 448
Qy	346 GEPLHHVDWARDGDP-----LEKLNVRLLPFENLSALLPGNFTGVGVPIRITTVASAGL 401
Dd	449 AAVQEYVVWV-RELHPGAGMQPPLGWLMSPPRYLSALISENIKPYICYEIRVHAL-AGDQ 506
Qy	402 ASASSWGPRELAPLVGPTLWRLODAPGCPATANGEVPRHQLRGLHTHTLTC---AQS 458

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Db 507 GGCNSTRGNSQKAPLSPGHINAISE-BKGSVLISWDEIPAREQMGCILHYRIWVKERDS 565
Qy 459 GTSPSVC-----MNVSGTQSVTLPLPMGCPCELWTAFTASTIAGQGGPPTILRLHLPDNTLRW 515
Db 566 NSQPOLCEIPYRISPNHPIBSLQ-PRVTVYLVMTALTAAAGESPQGNREFFCL-QGRANW 623
Qy 516 KVLPGILFLWGLFLGCGLSLATSGRCVHLRHKL-----PRWWEKVDPDPANSSGQPH 570
Db 624 STFVAPSIQMAVIMVG-----VLSMRCFQKVFVLLALRPQWCKEIPDPANSTWAKY 678
Qy 571 MEQVPEAQPLGDLFILE---VEEMEP-----PP-----VMSSQPAQA--T 606
Db 679 PIVEKTKQALDRLLTWTPTPEEPDELVINELCRVTPVFRPPHRSWSEKGGVQGHYT 738
Qy 607 APDLSGYEKHFLTP-----EBLGLLGP 629
Db 739 SEEDTGYSSASPPPPRAPTAFTGQGVLDLYKVLGSKGP 775

RESULT 8
Q6UANO PRELIMINARY; PRT; 870 AA.
AC Q6UANO;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Class I helical cytokine receptor number 26.
GN Name=CRFA26;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1];
RP SEQUENCE FROM N.A.
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blimont C., Skalli Z., Catolico L., Poulain J., Berardinis Vd.,
RA Cruaud C., Duprat S., Brottier C., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigs R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quirier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Crollius H.R.;
RA "Analysis of the Tetraodon nigroviridis genome reveals the
RT protokaryotype of bony vertebrates and its duplication in teleost
RT fish."
RL Nature 0:0-0(2004).
DR ENBL: AY174498; AAR25689.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS00853; FN3; 3.
KW Receptor.
SQ SEQUENCE 870 AA; 94718 MW; 6322B1618DC3E733 CRC64;

Query Match 8.9%; Score 313; DB 2; Length 870;
Best Local Similarity 22.8%; Pred. No. 3e-12;
Matches 151; Conservative 91; Mismatches 263; Indels 156; Gaps 29;

Qy 50 LNCSEWPLGDLGAPSELHLSQKYSNKTQTVAAV-----GRSWVAIPREQLTMSD 101
Db 137 MSCRWDPG-----RQTAAPTYTLTVAVRAVSNFVSVGTSGVPMVPVFFHM 187
Qy 102 KLLVW-----GTAKQPL-----WPPVFVNLETQMKNP-----RLGPDVDFSEDDPLE 146
Db 188 LLDIWVEARNILGTVESQHLQDAGW---FV-----KPPPSSELTILISEKSF-----PTS 234

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Qy 147 ATVWAPPTWPSHKVLICQFHYRRCOBAAWTLLEPELKTITPLTVEIQDLELATGYKVG 206
Db 235 LLSQWKHPIASVYMTLYEIRFAEADPGWTDVPAADTSKDIESFRLQKLRPDTLYTVQV 294
Qy 207 RCMEKEEDLWGWSPILSFQTP-----PSAPKDVVWSGNLCTPGGEBPLLLWKAAPGCVQ 263
Db 295 RCKYAHNGLHWSQMS-TKATRTPEDEKTSRPNWI---VAAPKQDRK-----GKWLQ 342
Qy 264 VSVKWFVWVGRELSPEGITCCCSLIPS-----CAEWARVSAVNATSW----- 306
Db 343 VVAKDPKFSNGK-----IOCFELEIQSLDEPLNPGAEWERTAVQAAPYDGRHLLK 396
Qy 307 -----EPLTNLSLVCLDSASA-----PRSVAVSSIAG----- 333
Db 397 QLLLPEGLSNVSVAVNSVGSASPVASLIIPKRTGGCGKARRGASTRTVGPLCAELPPV 456
Qy 334 -----STELLVTWQPGGEPL-EHVVDWARDGDPLEKLNWVRLPGNLSALLPNFT 384
Db 457 EDLEVRPRGRLRLWRPSSWRTASVYVWSSGAG-----WDMQRESRGTNTTLRGHLD 512
Qy 385 VGVPIRTTAVSASGLASASSVMGPREELAPLVGPTLMELODAPPCTPA-IANGEVPRH 443
Db 513 RFVCMISVPPYISRRRLGAPGSAQAQLEQAPLEGPAV-AVKDKPGHNEVELVWTEIPAH 571
Qy 444 QLRGHLTHYTLCAQSGTSPSCMNVSGNTQSVTLPLPMG-PCELWVTASTIAGQGGP 502
Db 572 QREGFITNYTIFYSSD-----ITVAANTSYTSLSSLSGNKYDAWVAVSTSAAR--PGA 623
Qy 503 ILRLHLPDNTLRWKVLPGLFLGGLSLATSGRCYHLRHKLPRWWEKVDP 562
Db 624 TTTTSPPTPGEVEAIVVVVCLLFFFLV-----LMATLLCIY-KEDTIKSLWPOINPG 677
Qy 563 NSSSG-----QPHWEQVPEAQPLGDLFILEVEEMEPVPMWESSQPAQATAPLSGY--EK 615
Db 678 ESTIGTWAPDYPLKAEPTKDGCVGSVSLAVDVCVQVRLEED---KAVLPLKDKYLSEE 734
Qy 616 H 616
Db 735 H 735

RESULT 9
GCSR HUMAN STANDARD; PRT; 836 AA.
ID _GCSR_HUMAN
AC Q39052; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)
DE (CD114 antigen).
GN Name=CSF3R; Synonyms=GCSFR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91079757; PubMed=2147944;
RA Larsen A., Davis T., Curtis B.M., Gimpe S., Sime J.E., Cosman D.,
RA Park L., Sorensen E., March C.J., Smith C.A.;
RT "Expression cloning of a human granulocyte colony-stimulating factor
RT receptor: a structural mosaic of hematopoietin receptor,
RT immunoglobulin, and fibronectin domains."
RL J. Exp. Med. 172:1559-1570(1990).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91062348; PubMed=1701053;
RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;
RT "Three different mRNAs encoding human granulocyte colony-stimulating
RT factor receptor."

```

Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).  
 [3] SEQUENCE FROM N.A.  
 RX MEDLINE=92091782; PubMed=1530796;  
 RA Seto Y., Fukunaga R., Nagata S.;  
 RT "Chromosomal gene organization of the human granulocyte colony-stimulating factor receptor.";  
 RL J. Immunol. 148:259-266(1992).  
 [4] SEQUENCE FROM N.A., AND VARIANTS THR-231; ASN-320; ARG-346; LYS-405; GLN-440; HIS-510; HIS-562 AND CYS-583.  
 RP Rieder M.J., Armet T.J., Carrington D.P., Ozuna M., Kuldaneck S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
 RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [5] SEQUENCE FROM N.A. (ISOFORM 1).  
 RP TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Riedel M.J., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6] DOMAINS STRUCTURE.  
 RP MEDLINE=92007729; PubMed=1717255;  
 RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;  
 RT "Functional domains of the granulocyte colony-stimulating factor receptor.";  
 RL EMBO J. 10:2855-2865(1991).  
 [7] DISEASE.  
 RX MEDLINE=94240159; PubMed=7514305;  
 RA Dong F., Hoeflloot L.H., Schelen A.M., Broeders C.A., Meijer Y., Veerman A.J., Touw I.F., Lowenberg B.;  
 RT "Identification of a nonsense mutation in the granulocyte colony-stimulating factor receptor in severe congenital neutropenia.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4480-4484(1994).  
 [8] STRUCTURE BY NMR OF 227-334.  
 RP MEDLINE=97331327; PubMed=9187659;  
 RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;  
 RT "Solution structure of an extracellular domain containing the WSxWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand.";  
 RL Nat. Struct. Biol. 4:498-503(1997).  
 [9] 3D-STRUCTURE MODELING OF 125-331.  
 RP MEDLINE=98037802; PubMed=9368043; DOI=10.1074/jbc.272.47.29735;  
 RA Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;  
 RT "Identification of a ligand-binding site on the granulocyte colony-stimulating factor receptor by molecular modeling and mutagenesis.";  
 RL J. Biol. Chem. 272:29735-29741(1997).  
 CC -1- FUNCTION: Receptor for granulocyte colony-stimulating factor. In addition it may function in some adhesion or recognition events at the cell surface.

CC -1- SUBUNIT: Dimer (Probable).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Isoform GCSFR2, which lacks the transmembrane domain, may represent a soluble form of the receptor.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Comment=Additional isoforms seem to exist. Experimental confirmation may be lacking for some isoforms;  
 CC Name=1; Synonyms=GCSFR-1;  
 CC IsoId=G99062-1; Sequence=Displayed;  
 CC Name=2; Synonyms=GCSFR-2;  
 CC IsoId=G99062-2; Sequence=VSP\_001674;  
 CC Name=3; Synonyms=GCSFR-3;  
 CC IsoId=G99062-3; Sequence=VSP\_001673;  
 CC Name=4; Synonyms=GCSFR-4, D7;  
 CC IsoId=G99062-4; Sequence=VSP\_001671, VSP\_001672;  
 CC -1- TISSUE SPECIFICITY: One or several isoforms have been found in myelogenous leukemia cell line KG-1, leukemia U937 cell line, in bone marrow cells, placenta, and peripheral blood granulocytes. Isoform GCSFR-2 is found only in leukemia U937 cells. Isoform GCSFR-3 is highly expressed in placenta.  
 CC -1- DOMAIN: The WSxWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.  
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or activation.  
 CC -1- DISEASE: Defects in CSF3R might be a cause of severe congenital neutropenia (SCN) in some patients.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 2.  
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD114 entry;  
 CC WWW=<http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm>.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 CC EMBL; X55721; CAA39253.1; -  
 CC EMBL; X55720; CAA39252.1; -  
 CC EMBL; S71484; AAB20860.1; -  
 CC EMBL; M59818; AAA63176.1; -  
 CC EMBL; M59819; AAA63177.1; -  
 CC EMBL; M59820; AAA63178.1; -  
 CC EMBL; AY148100; AAN05790.1; -  
 CC EMBL; BC053585; AAB53585.1; -  
 CC PIR; B38252; B38252.  
 CC PIR; C38252; C38252.  
 CC PIR; JH0329; JH0329.  
 CC PDB; 1AZ7; Model; @=125-331.  
 CC Genew; HGNC:2439; CSF3R.  
 CC MIM; 138971; -  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004872; F:receptor activity; TAS.  
 CC GO; GO:0006952; P:defense response; TAS.  
 CC InterPro; IPR002996; Cytokn\_recept\_B/G.  
 CC InterPro; IPR003961; FN\_III.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003529; Hemtrecept\_1302.  
 CC InterPro; IPR010457; Lep\_receptor\_Ig.  
 CC Pfam; PF00041; fn3; 3.  
 CC Pfam; PF06328; Lep\_receptor\_Ig; 1.  
 CC PROSITE; PS00853; FN3; 5.  
 CC PROSITE; PS01353; HEMATOPO\_REC\_L\_P2; 1.  
 CC 3D-structure; Alternative splicing; Cell adhesion; Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 24

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FT CHAIN 25 836 Granulocyte colony stimulating factor
FT FT receptor.
FT FT Extracellular (Potential).
FT TRANSMEM 627
FT DOMAIN 650
FT DOMAIN 651 836
FT DOMAIN 651 836
FT DOMAIN 117
FT DOMAIN 122 222
FT DOMAIN 237 330
FT DOMAIN 334 426
FT DOMAIN 430 522
FT DOMAIN 527 618
FT SITE 318 322
FT SITE 658 666
FT DISULFID 131 142
FT DISULFID 248 295
FT DISULFID 266 309
FT CARBOHYD 51 51
FT CARBOHYD 93 93
FT CARBOHYD 128 128
FT CARBOHYD 134 134
FT CARBOHYD 389 389
FT CARBOHYD 474 474
FT CARBOHYD 579 579
FT CARBOHYD 610 610
FT VARSPLIC 750 783

Query Match 8.5%; Score 297.5; DB 1; Length 836;
Best Local Similarity 22.8%; Pred. No. 3.1e-11;
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

Qy 50 LNCSEPLDGLGAPSELHLSQKYSR-N-KTQTVAV-----AAGRSWVAIPREQLTMSDKL 103
Db 140 LICQWEPGPEHPTSLTSLKFSKRGNCQIQGSDILCVKQDQSHCCIPKHLHLLQNM 199

Qy 104 LVW-----GTXAGQPLW-----PPVFNLETQMKPNAPRLG-----PDVDF 139
Db 200 GIWVQAEALGTSMSPOLCLDPMVDVVKLEPPMLRTMDPSPEAAPQAGCLQCWEP----- 255

Qy 140 SEDDPLEATVHAPPTWPSHVKLQCF-HYRRCQEAATWLLPELKTIPLTPTVEIQDEL 198
Db 256 -----WQGLHINQK---CELRHPQGEASWALVGP-----LPLEALQYEL 294

Qy 199 -----ATGYKYVGRCKMEEDLWGEWSPILSFQTPPSAPK---DVMVSGNLGCTPGGEE 250
Db 295 CGLLPATAYTLQIRCIWPLPGHSDWSPSLELRTTERRAFTVRLDTW----- 341

Qy 251 PLLLWKAPGCVQSVYKVFVWVGRELSPGICITCCCSLIPSGAEWARSVAVNATSWEP-- 308
Db 342 ---WRQ-----RQLDPRTVQLFWKPVPLEEDSGRIQGY-VVSWRPSG 379

Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
Db 380 QAGAILPLCNTELSCTHFLPSEAEVALVAYNSAGTSRTPVVFSESRGPAITRIHAMA 439

Qy 336 -----ELAVTWQPGGEPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGP 388
Db 440 RDPHSLWGVGEPNPNWPGQVIEWGLGPPSASNSKTRMEQNGRATGFLLENIRPQL 499

Qy 389 YRITVTAVSAGLASASSVNGFREELAPLVGPTLWRLQDAPGTPATAWGEVPRHQLRGH 448
Db 500 YEIIVTPLYQDTWGPSQHVYAYSQEMAPSHAPEL-HLKHTGKTWQAEWPEPEPELGKSP 558

Qy 449 LTHVTLCAQSGTSPVCMVNSGNTQSVTLPLDMPGCELM-----VTA 491
Db 559 LTHYITFWTAQNSQSFSAIINASSRGVFLHGLE--PASLYHIHLMASQAGATNSTVLT 616

Qy 492 STIAGQPPGPIRLRLHLPDNTLRWKVLPGLFLWGLFLL---GGLSLATSGRCYHLRHK 548
Db 617 MTLTPEG-----ELHI-----ILGFLGLLLLTCLCG-----TAWLCCSPNRK 655

Qy 549 VLRVWVWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPILEVEEMPPPPVMS 599
Db 656 ---NPLWPSVDPDAHSSLSGWSVPTIMEEDAFQLPGLGTPITKLTVLEEDKKVPV-WES 711
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Qy 600 SQPAQATAPLDSGYEKHFLPTPELGLL-GPPR 631
Db 712 HNSSETCG-----LFTLVQTYVLQGDPR 734

RESULT 10
Q65214 PRELIMINARY; PRT; 962 AA.
ID Q65214
AC Q65214
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Oncostatin M specific receptor.
GN Name=OSMR;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Okaya A., Kitanaka J., Kitanaka N., Satake M., Terada K., Sugiyama T.,
RA Takemura M., Fujimoto J., Terada N., Miyajima A., Tsujimura T.;
RT "Rat oncostatin M specific receptor mRNA."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB167522; BAD44758.1; -.
KW Receptor.
SQ SEQUENCE. 962 AA; 108624 MW; A7A15FED59A6E21A CRC64;

Query Match 8.5%; Score 296; DB 2; Length 962;
Best Local Similarity 24.0%; Pred. No. 4.6e-11;
Matches 166; Conservative 75; Mismatches 283; Indels 168; Gaps 37;

Qy 50 LNCSEPLDGLGAPSEL--HLQ-SQYR-----SNKTQTVAVAGRSWVAIPREQLTMSD 101
Db 251 LNCLEWP-----GIDTTLWSHKQSRQSHYTLYESPSGRREVSNHRNSTWQITDSQETYNF 306

Qy 102 KLLVWGTKAGOLPWPVFVNLETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKV 161
Db 307 TLTAENNLKRSV--SISFNLTHRVHPKAPH---DVTLKTVGATKAHMTWKVPSRGDY-T 360

Qy 162 LICQFYHRCQEAATWLLPELKTIPLTPTVEIQDELATGKYVGRCKMEEDLWGEWS 221
Db 361 LLCQVEL-QCE--GEVIHEHNSVHTSANVLFSDLEPDIYKACVRCASANHFWKNSDWM 417

Qy 222 PILSFQTPPSAPK---DVMVSGNLGCTPGGE-----BPLLWKAPGCVQSVYKVFVW 271
Db 418 Q-KKFRTPPEAPSEALDVRD---VRTENGRHVVTLVFWKPLKSOANGKI--ISYNI--- 468

Qy 272 VGGRELSP-----GITCCCSLIPSGAEWARSVAVNATSWEPITNLSLCLDS 319
Db 469 VVENEANPTESEQYSVRAPALGNLSLDLHPYK---IHISANNASAGASP---BSLVVLS 522

Qy 320 ASAPRSVAVSSIAG-STELLVTWQPGGEPLEHVVDWARDGDPLE-KLNWVRLPPGNLSA 377
Db 523 HSGHEEVHEKTIKIKNGFNISWEPVSGDAIGVVDWCAHSQTCRCDLQWKNVGNITST 582

Qy 378 LIPGN-FTVGVPIRITVAVSA-SGLASASSVNGFREELAPLVGPTLWRLQDAPGTPAI 435
Db 583 IITSDAFEPGVYRIFERSVEENVRLVEKQGYTQELAPSVNPGV-TIHNLTPNSFSL 641

Qy 436 AM-----GEVPRQLRGLHLY-----TLCAQSGTSPVCMVNSGN 471
Db 642 KWQDYASDFQSGFIKGYLVLYLSKELQCNPNWERTVLSDKSVLCCKYDVDDP-----E 693

Qy 472 TQSVTLPLDL-PWGPCELWWTASTIAQGGPPGPIRLHLPD---NTLRWKVLPGLFLWGL 527
Db 472 TQSVTLPLDL-PWGPCELWWTASTIAQGGPPGPIRLHLPD---NTLRWKVLPGLFLWGL 527
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Db 694 TKTLAVENLRPSLYEFLVTPYTSAGQGNETYTKVTTPDVRSHMLLQIILP----- 745
QY 528 FLGCGLSLATSGRCVHLRHKVLPRVWEK-----VPDPANSS----- 565
Db 746 MTLGVFLSIIV---CYW-----KSQWKEKCYDPIDPNPYKSSILSLIKSKNPHLIMNVK 797
QY 566 -----SGOPHMEQVPEAQLGDLPLILEVEEMEPVPMESSQPA 603
Db 798 DCIPDVLEINKAEGSKTCVSGKLHEDVTKEPL--VP-TEKDSSGPFVLENFPT 854
QY 604 QATAPLDSGYEKHFLP-----TPBELGLLGGP 630
Db 855 YDQSAFDSG-SHGFTPGPLKNTPHQLGLLAPP 885

RESULT 11
ID O70458 PRELIMINARY; PRT; 971 AA.
AC O70458;
DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Oncostatin M specific receptor.
GN Name=Osmr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252923; PubMed=9584176;
RA Lindberg R.A., Juan T.S., Welcher A.A., Sun Y., Cupples R.,
RA Guthrie B., Fletcher F.A.;
RT "Cloning and characterization of a specific receptor for mouse
RT oncostatin M."
RL Mol. Cell. Biol. 18:3357-3367(1998).
DR EMBL; AF058805; AAC40122.1; -.
DR MGD; MGI:1330819; Osmr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004924; F:oncostatin-M receptor activity; IDA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR002996; Cytln recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003529; Hemtrecept_1302.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 971 AA; 110229 MW; BECA085BBD47C1E7 CRC64;

Query Match
Best Local Similarity 22.9%; Pred. No. 8.5e-11;
Matches 159; Conservative 87; Mismatches 275; Indels 174; Gaps 34;

QY 50 LNCSEPLDGLAPSLHLQSKYR-----SNKTQVAVAGRSWVAIPREQ----- 96
Db 250 LDCSEWP-----GVDTLTWKRFQNYLTCSFSKRCVSNYSYTWQITGSQEMYNF 305
QY 97 -LTMSDKLLVWGTKAGQPLPVPFVNLETOMKPNAPRLGPDVDFSDDEPLEATVHWAPPT 155
Db 306 TLTAENQLKRSVN-----INFNLTHRVHPKAPQ---DVTLKIGATKANWYKHS 354
QY 156 WPSHKYLIQCFHYRRCQEAWTLLEPELKIPLTPVEIQDLELATGYKYVGRCRMEKED 215
Db 355 HGNVYTLQCQVKLQYGE---VTHEHNSVHMSANYLFSDDLDPDTKYKAFVRCASANHF 410
QY 216 LMGWSPILSFQTPPSAPK---DVWVSGNLGTFPGSEEPILLWKAPGVCVQ-----VS 265
Db 411 KWSDMTQK-KEFSTPETAPSQALDW--RQVWSENGRRIVTLFWK---PLLKSOANGKIIS 464
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QY 266 YKVMFWVGRELSPEGITCCSLIPSGAWEA-----RVSAVNATSWEP 309
Db 465 YNI---VVENEAKPTSEHYC-----VMAPALSTNLSLDLPYKIRITTNNSMGASP- 513
QY 310 TNLISLVCLDSASAPRSVAVSSIASTELL-VTWQPGCGEPLEHVVDW-ARDGDPLEKLNW 367
Db 514 --ESLWLSNDSGHEEVKEKTIKGIKDAFNISWEPVSGDTMGYYVDWCAHSQDQRCDLQW 571
QY 368 VRLPPGNLSALLPG-NFTVGPYKRTITVAVSAGLAS-ASSVWGFRFELAPLVGPTLWRL 425
Db 572 KNLGNTTSTTITSDDFKPGVRYNFRIPERSVEHKARLVEKQRTQBLAELVNPKV--- 628
QY 426 QDAPEGTP---AIANGVEPRHQLRHLTHYTLCAQS-----GTSPSCVN 467
Db 629 -EIPYSTENSFVLWPDYDSDFQAGFIKGYLVVYKSKEMQCNPQWERTLLPDNSVLCKYD 687
QY 468 VSGN-TQSVTLDDL-PWGPCELWVTASTIAGGPGPILRLHLPDNTLRWKLPGILFLW 525
Db 688 INGSETKLTVENLQPELSLEYEFFVTPTYSAGPGNETFTKVTTPD--ARSHMLLQIILPM 745
QY 526 GLFLGCGLSLATSGRCVHLRHKVLPRVWEK-----VPDPANSS----- 565
Db 746 TLCVL---LSIIV---CYW-----KSQWKEKCYDPIDPNPYKSSILSLIKSKNPHLIMN 794
QY 566 -----SGOPHMEQVPEAQLGDLPLILEVEEMEPVPMESSQ 601
Db 795 VKDCIPDVLEINKAEGSKTCVSGKLHIEDVTPKPI--VP-TEKDSSGPFVPCIFPEN 851
QY 602 PAQATAPLDSGYEKHFL-----TPBELGLLGGP 630
Db 852 FTYDQSAFDSG--SHGLIPGLKDTAHLGLLAPP 884

RESULT 12
O88821 PRELIMINARY; PRT; 970 AA.
ID O88821;
AC O88821;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Oncostatin M receptor beta.
GN Name=Osmr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120951; PubMed=9920829;
RA Tanaka M., Hara T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Miyajima A.;
RT "Reconstitution of the functional mouse oncostatin M (OSM) receptor:
RT molecular cloning of the OSM receptor beta subunit."
RL Blood 93:804-815(1999).
DR EMBL; AB015978; BAA33725.1; -.
DR MGD; MGI:1330819; Osmr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004924; F:oncostatin-M receptor activity; IDA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR002996; Cytln recept_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003529; Hemtrecept_1302.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 970 AA; 110070 MW; E3A07D41754FA847 CRC64;

Query Match
Best Local Similarity 22.6%; Score 288.5; DB 2; Length 970;
Pred. No. 1.4e-10;
```



	MEDLINE=97331327; PubMed=9187659;
RX	Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RA	"Solution structure of an extracellular domain containing the WSxWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand";
RT	Nat. Struct. Biol.
RL	4:498-504(1997).
CC	-! FUNCTION: Receptor for granulocyte colony-stimulating factor. In addition it may function in some adhesion or recognition events at the cell surface.
CC	-! SUBUNIT: Dimer (Probable).
CC	-! SUBCELLULAR LOCATION: Type I membrane protein.
CC	-! TISSUE SPECIFICITY: Found in bone marrow.
CC	-! DOMAIN: The WSXS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
CC	-! DOMAIN: The box 1 motif is required for JAK interaction and/or activation.
CC	-! SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 2.
CC	-! SIMILARITY: Contains 5 fibronectin type III domains.
CC	-! SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M58288; AAA37673.1; --
DR	PIR; A34898; A34898.
DR	PDB; 1CD9; X-ray; B/D=120-334.
DR	PDB; ICTO; NMR; @=211-333.
DR	PDB; LCGF; NMR; @=211-333.
DR	PDB; LPGR; X-ray; B/D/F/H=120-334.
DR	MGD; MG1:1339755; Csf3r.
DR	GO; GO:0030593; P:neutrophil chemotaxis; IMP.
DR	InterPro; IPRO02996; Cytkn recept_B/G.
DR	InterPro; IPRO03961; FN_III
DR	InterPro; IPRO08957; FN_III-like.
DR	InterPro; IPRO03529; Hemtrecept_L102.
DR	InterPro; IPRO10457; Lep_receptor_Ig.
DR	pfam; PF00041; fn3; 3.
DR	Pfam; PF06328; Lep_receptor_Ig; 1.
DR	PROSITE; PS50853; FN3; 5
DR	PROSITE; PS01353; HEMATOPD_REC_L_F2; 1.
KW	3D-structure; cell adhesion; Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal; Transmembrane.
KM	SIGNAL
FT	1       25        Potential.
FT	CHAIN          26    837    Granulocyte colony stimulating factor receptor.
FT	DOMAIN          26    626    Extracellular (Potential).
FT	TRANSMEM      627    650    Potential.
FT	DOMAIN         651    837    Cytoplasmic (Potential).
FT	DOMAIN          26    118    Ig-like C2-type.
FT	DOMAIN         123    223    Fibronectin type-III 1.
FT	DOMAIN         231    328    Fibronectin type-III 2.
FT	DOMAIN         330    429    Fibronectin type-III 3.
FT	DOMAIN         431    525    Fibronectin type-III 4.
FT	DOMAIN         527    621    Fibronectin type-III 5.
FT	SITE     319    323    WSXS motif.
FT	SITE     658    666    Box 1 motif.
FT	DISULFID      132    143    By similarity.
FT	DISULFID      249    296    By similarity.
FT	DISULFID      267    310    By similarity.
FT	CARBHYD       51    51     N-linked (GLCNAC..?) (Potential).
FT	CARBHYD       94    94     N-linked (GLCNAC..?) (Potential).
FT	CARBHYD      129    129    N-linked (GLCNAC..?) (Potential).
FT	CARBHYD      186    186    N-linked (GLCNAC..?) (Potential).
FT	CARBHYD      279    279    N-linked (GLCNAC..?) (Potential).
FT	CARBHYD      392    392    N-linked (GLCNAC..?) (Potential).
FT	CARBHYD      408    408    N-linked (GLCNAC..?) (Potential).

FT	CARBOHYD	474	474	N-linked (GlcNAc. . .)	(Potential)	
FT	CARBOHYD	487	487	N-linked (GlcNAc. . .)	(Potential)	
FT	CARBOHYD	582	582	N-linked (GlcNAc. . .)	(Potential)	
FT	CARBOHYD	613	613	N-linked (GlcNAc. . .)	(Potential)	
FT	STRAND	128	135			
FT	TURN	136	139			
FT	STRAND	140	146			
FT	STRAND	156	163			
FT	HELIX	166	188			
FT	STRAND	174	179			
FT	STRAND	186	190			
FT	HELIX	191	193			
FT	TURN	196	197			
FT	STRAND	200	208			
FT	TURN	209	210			
FT	STRAND	211	214			
FT	STRAND	218	220			
FT	HELIX	222	224			
FT	STRAND	226	226			
FT	STRAND	232	235			
FT	STRAND	250	255			
FT	HELIX	258	260			
FT	TURN	261	262			
FT	STRAND	265	273			
FT	TURN	276	277			
FT	STRAND	281	287			
FT	STRAND	290	295			
FT	STRAND	304	312			
FT	STRAND	326	328			
SQ	SEQUENCE	837 AA;	93406 MW;	42295989E2C8531 CRC64;		
Query Match 7.9%; Score 277; DB 1; Length 837;						
Best Local Similarity 24.2%; Pred. No. 7e-10;						
Matches 172; Conservative 83; Mismatches 295; Indels 162; Gaps 37;						
QY	32	POGSAGPLQCYGVGLDNCSEWPEGLDGLGAPSELHLQSKYRSN-----KTQTVAAGAAG 86				
Db	123	PPASPSNLSCMLHLLTNSLVCQWEPGPEHLPSTFSLKSRADQCYQGDITPCVAKK 182				
QY	87	R-SWVAIPREQLTMSDKLVW-----GKAGQPLW--PPVFNLETKMKNAPRLGPD 136				
Db	183	RONNCISPRKLLLYQYMAIWOAENMLGSSSPKCLDPMVVKLEPML-QALDIGPD 241				
QY	137	VDFSEDDPLEATVHMAPPYTPWPSKVL--ICQFYR-RCQEAATWLL--EPLEKTIPLTPV 191				
Db	242	V--VSHQPGCLWLSWKP--WKPEYMEQECELRYQQLKGANWLVFLPSSK----DQF 293				
QY	192	EIQDLELATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPK---DVMVSGNLCGTPCG 248				
Db	294	ELCGLHQAQVYTLQMRICRSLPGFSPWSPGLQLRPTWKAPTIRLDTWCOKQL-DPGT 352				
QY	249	EEPELLWKAPGPCVQVSYKWFVW-----CGRELSPEGIT--CCCSLIPSGAEWARV 298				
Db	353	VSQVLFWK-FTPLQEDSGQIQGYLLWNPSDPHQDHLNNTQLSCIFLLPSEAQ---- 407				
QY	299	SAVNATSWPELTNLSLCLDSA--SAPRSV-----AVSSIAGSTE-----LLVTWQPC 344				
Db	408	-----NVLVAYNKAGTSSTTVTVFLENGEPAVTGLHAMAQDLNTIWDWEAP 455				
QY	345	PGEPLEHVVDWARDGDPLEK--LNWRLPPGNLSA-LLPGNFTVGVPIRYITVAVSAGL 401				
Db	456	SLLPQGYLIEWESSPSYNNYSKSWMEIPENGNITGILLKDNINFPQLYRITVAPLYPGIV 515				
QY	402	ASASSVWGFEELAPLVGP-----TLWRLQDAPGTEPAIANGVPRHQLRHLTHYT 453				
Db	516	GPPNVVTFAGEAPPHAPALHLKHVGTWQAQLEWPEAPRL--GMIP-----LTHYT 566				
QY	454	L-CAQSGT-SPSVMVSGNTQSVTLPLD--PWGCELWVTASTIAGQ-GPPGPIRLHLHP 509				
Db	567	IFWADAGHSFVTLNIS--LHDFVLKHLSPASLYHVLYMATSKAGSTNSTGLTLATLDP 624				
QY	510	DNTLRWKLPGILPLGCLLFLGCLSLATGRCVHLRHKVLPRWVKEKVDPANSS----- 565				

Db	625	SDL-----NIFLGILCLVLLSTTCVTVWLCKRRGKTS----FWSVDVDPDAHSSLSW 673				
QY	566	-----SGOPHMEQVPEAQP-----LGDLPIL---EVEEME 592				
Db	674	LPTMTETQLPSFWDSSVPSITKITELEBEDKPTHWDSESSNGSLPALVQAVVLQGD 733				
QY	593	PPVMESSQPAQATAPLDGSEKHFLETPBELG-----LLGPPRP 632				
Db	734	PREISNQSPSRGTG--DQVLYGQVLESPTSPGVWQVIRSDSTQPLLGPTP 783				
RESULT 14						
IL6B HUMAN						
ID	IL6B HUMAN	STANDARD;	PRT;	918 AA.		
AC	P40189; Q9U041;					
DT	01-FEB-1995 (Rel. 31, Created)					
DT	01-FEB-1995 (Rel. 31, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin					
DE	6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M					
DE	receptor) (CD130 antigen).					
GN	Name=IL6ST;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORM 1).					
RC	TISSUE=Myeloma, and Placenta;					
RX	MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;					
RA	Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;					
RT	"Molecular cloning and expression of an IL-6 signal transducer,					
RT	gp130.";					
RL	Cell 63:1149-1157(1990).					
RN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORM 2).					
RC	TISSUE=Synovium;					
RX	MEDLINE=20341529; PubMed=10880057;					
RA	Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,					
RA	Murakami M., Nakao K.;					
RT	"Cloning of novel soluble gp130 and detection of its neutralizing					
RT	autoantibodies in rheumatoid arthritis.";					
RT	J. Clin. Invest. 106:137-144(2000).					
RN	[3]					
RP	PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.					
RX	MEDLINE=21269388; PubMed=11098061; DOI=10.1074/jbc.M009979200;					
RA	Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;					
RT	"Determination of the disulfide structure and N-glycosylation sites of					
RT	the extracellular domain of the human signal transducer gp130.";					
RL	J. Biol. Chem. 276:8244-8253(2001).					
RN	[4]					
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.					
RX	MEDLINE=98169383; PubMed=9501088; DOI=10.1093/emboj/17.6.1665;					
RA	Bravo J., Staunton D., Heath J.K., Jones E.V.;					
RT	"Crystal structure of a cytokine-binding region of gp130.";					
RL	EMBO J. 17:1665-1674(1998).					
CC	-!- FUNCTION: Signal-transducing molecule. The receptor systems for					
CC	IL6, IL6, IL6, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating					
CC	signal transduction. Binds to IL6/IL6R (alpha chain) complex,					
CC	resulting in the formation of high-affinity IL6 binding sites, and					
CC	transduces the signal. Does not bind IL6. May have a role in					
CC	embryonic development (by similarity). a beta chain.					
CC	-!- SUBUNIT: Heterodimer of an alpha and a beta chain.					
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).					
CC	Secreted (isoform 2).					
CC	-!- ALTERNATIVE PRODUCTS:					
CC	Event-Alternative splicing; Named isoforms=2;					
CC	Name=1;					
CC	isoID=P40189-1; Sequence=Displayed;					
CC	Name=2; Synonyms=Gp130-RAPS;					
CC	isoID=P40189-2; Sequence=VSP 001684, VSP 001685;					
CC	-!- TISSUE SPECIFICITY: Found in all the tissues and cell lines					
CC	examined. Expression not restricted to IL-6 responsive cells.					



```
Db 361 GKILDY-----VLTTRWKSHLQNTVNTATKLTVLNLTNDRLATL 400
Qy 327 AVSSAGSTELLATVWPGCEPLEHV-----VDWADGDPLEK--LNNVRL 370
Db 401 TVRNLVGKSDAAVLTPACDFQATHPVMDLKAPKDNMLWVETTPRESVKKYILEWCVL 460
Qy 371 -----PPGNL-SALPGNFTVGPVYRITVAVSAGLASASSVMGFRELAPL 417
Db 461 SDKARCITDQOEDGTGVTYRLGNLAESKYLITVTPYADGPGSPSIIKAYLKQAPPS 520
Qy 418 VQPTLWRLQDAPPGTAPTAANGVPRHQLRHGTHYTLCAQSGTSPSCVMNVSNGTQSVTL 477
Db 521 KGFTV-RTKKVGKNEAVLEWDQLPVDVQNGFTFRNTVTFYRTIIGNETAANVDSSTHTVTL 579
Qy 478 PDLPGPCELWNTASTIAGQPPGPIILRLHP-----DNTLRWVKVLPGLFLWGLFLILGCL 534
Db 580 SSLTSDTLVYVMAAYTDEGGKDGPEFTFTTKPAQGEIATVVPCL-----AFLLTTL 635
Qy 535 SLATSGRCVHLRHVKVLPVWWEKVPDPANSSGQ--PH-----MEQVPEAQPLGDL 583
Db 636 GVLF---CFNKR-DLKKHINVPDPKSHIAQWSPHTPPRHNFNSKDMQYSDGNFTDV 691
Qy 584 PILEVEEMEP-----VMESSQPA----- 603
Db 692 SVVEIENDKFPEDLKSLLDKKEKINTEGHSGIGGSCWSSSRPSISSDENESSQ 751
Qy 604 -----QATPLDSGYEKHFLPT-----PEBLGLL 627
Db 752 NTSSTVQVSTVHSGY-RHQPVSQVFSRSESTQPLDSEERPEDLQLV 799

RESULT 15
IL6B_MOUSE
ID IL6B_MOUSE STANDARD; PRT; 917 AA.
AC Q00560;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN Name=Il6st;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal
transducer, gp130, and its regulated expression in vivo.";
RL J. Immunol. 148:4066-4071(1992).
CC -!- FUNCTION: Signal-transducing molecule. The receptor systems for
CC IL6, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating
CC signal transduction. Binds to IL6/IL6R (alpha chain) complex,
CC resulting in the formation of high-affinity IL6 binding sites, and
CC transduces the signal. Does not bind IL6. May have a role in
CC embryonic development.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found in tissues such as brain, heart, thymus,
CC spleen, kidney, lung and liver. Found in all the cell lines tested
CC except BAF-B03. Expression not restricted to IL6-responsive cells.
CC -!- DEVELOPMENTAL STAGE: In embryonic stem cells it is found from day
CC 6 of gestation. It reaches a peak on day 8 and gradually declines
CC during the rest of embryogenesis.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
```

```
CC Subfamily 2.
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X62646; CAA44515.1; -.
CC EMBL; M83336; AAA37723.1; -.
CC PIR; I49699; I49699.
CC HSP; P40189; IBOU.
CC MGI; MGI:96560; Il6st.
CC GO; GO:0008593; P:regulation of Notch signaling pathway; IDA.
CC GO; GO:0007165; P:signal transduction; IDA.
CC InterPro; IPR002996; CytKn_recept_B/G.
CC InterPro; IPR003961; FN_III-like.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003529; Hemtrecept_1302.
CC InterPro; IPR010457; Lep_receptor_Ig.
CC Pfam; PF00041; fn3; 4.
CC Pfam; PF06328; Lep_receptor_Ig; 1.
CC PROSITE; PS50853; FN3; 5.
CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
CC Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 917 Interleukin-6 receptor beta chain.
FT DOMAIN 23 617 Extracellular (Potential).
FT TRANSMEM 618 639 Potential.
FT DOMAIN 640 917 Cytoplasmic (Potential).
FT DOMAIN 26 120 Ig-like C2-type.
FT DOMAIN 125 214 Fibronectin type-III 1.
FT DOMAIN 220 319 Fibronectin type-III 2.
FT DOMAIN 324 416 Fibronectin type-III 3.
FT DOMAIN 421 512 Fibronectin type-III 4.
FT DOMAIN 514 608 Fibronectin type-III 5.
FT DOMAIN 723 741 Ser-rich.
FT SITE 308 312 WSXWS motif.
FT SITE 649 657 Box 1 motif.
FT DISULFID 28 54 By similarity.
FT DISULFID 48 103 By similarity.
FT DISULFID 134 144 By similarity.
FT DISULFID 172 180 By similarity.
FT DISULFID 456 464 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 131 131 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 225 225 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 388 388 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 551 551 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 917 AA; 102452 MW; FCFD220BC2466F4 CRC64;

Query Match 7.1%; Score 248; DB 1; Length 917;
Best Local Similarity 21.1%; Pred. No. 6,5e-08;
Matches 140; Conservative 85; Mismatches 253; Indels 186; Gaps 27;
Qy 107 GTKAGQPLWPPVFNLETFQMK-PNAPRIG-----PDVSEDDPLEATVHWAPP----- 154
Db 177 GTSCVMVSYMTYVNIWVEAENA--LGKVSSESINFPDVKVKT----PPYNLSVTN 230
Qy 155 -----TWPSHKV-----LIQFHYRRCQEAATLLPELKTIPLTVPVFIQDELA 199
Db 231 SEELSSIIKLWSVSGGLGLDLKSDIQYRTKDASTWIOVPLEDTNSPTSTVQDLKPF 290
Qy 200 TGYKVYGRCMKEKEDLWGEWSPILS----FQTPPSAPKDVWVSGNLGCTPGGEPFLLMK 256
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Db 291 TEYVFRIRSIKDSKGKGYWSDWSEASCTTYEDRSPRPSPFWYKTNPSHGQYRSVRLIWK 350  
Qy 257 APGPCVOVSVKV-----WFWVGGRELSPE-----GITCC 285  
Db 351 AL-PLSEANGKILDYEVILTQSKSVSQTYVTGTTELTNTNDRIYASLAARNKVGKSA 409  
Qy 286 CSL-IPSGAEWARVSAVNATSWBELTNLSLVCLDSASAPRSVAVSSIAGSTELLVWQPG 344  
Db 410 AVLTIPSPHVTAAYSVVNLKAP-PKDNL-----LWVEWTPP 444  
Qy 345 PGEPLEHVVDWA--RDGDPLEKLNWVRLPPGNLSALLPGNFTVGVPIRYITVAVSAGLA 402  
Db 445 PKPVSKYILEMCVLSENAPCBE-DWQOEDATVNRTHLRGLLESKCYQITVTPVFATPG 503  
Qy 403 SASVVMGFREELAPLVGPTLWRLQDAPPGTPATAWGEVPRHQLRGLHLYTLCAGSTSP 462  
Db 504 GSESLKAYLKQAPARGPTV-RTKKVGKNEAVLAWDOI PVDDQDQGFIRNYSISYRTSVGK 562  
Qy 463 SVCNMVSGNTQSVTLPLDPLWGPCELWVTASTIAGQGPPIRLHLFP---DNTLRWKVLP 519  
Db 563 EMVVHVDSSHTEYTLSSSDTLVMVRMAAYTDEGKDGPEFTTTPKPAQGEIEAIVP 622  
Qy 520 GILPLWGLFLGCGLSLATSGRCVHLRHVLPVWVWEKVPDPDANSSGQ--PH----- 570  
Db 623 VCL-----AFLTLTLLGVLF--CFNKR-DLIKKHIWPNVDPSPKSHIAQWSPHTPPRHN 674  
Qy 571 --MEQVPEAQPLGDLPILEVEEMEPPP-----VMES 599  
Db 675 NSKDMYSNGNFTDVSVEIEANNNKPCDDDLKSVDLFKKEKSVTEGHSSGIGSSCMSS 734  
Qy 600 SQP-----AQATAP-----LDGYEKHFLPT-----PEE 623  
Db 735 SRPSSISNEENESAQSTASTVEYSTVHSCY-RHQVPSVQVPSRSESTQPLLDSEERPED 793  
Qy 624 LGLL 627  
Db 794 LQLV 797

Search completed: February 19, 2005, 01:16:02  
Job time : 186 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2005, 01:07:42 ; Search time 43 Seconds  
(without alignments)  
1104.112 Million cell updates/sec

Title: US-10-088-950A-1  
Perfect score: 3498  
Sequence: 1 MRGGRGAPFWLPLKALL.....FLPTPELGLGPPRPQVLA 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	1	US-08-653-740-5
2	3498	100.0	636	2	US-09-073-594-5
3	3498	100.0	636	3	US-09-275-925-5
4	3150	90.1	578	1	US-08-653-740-3
5	3150	90.1	578	2	US-09-073-594-3
6	3150	90.1	578	3	US-09-275-925-3
7	2044	58.4	623	1	US-08-653-740-7
8	2044	58.4	623	2	US-09-073-594-7
9	2044	58.4	623	3	US-09-275-925-7
10	380	10.9	862	2	US-08-685-118-2
11	380	10.9	862	2	US-08-915-495-2
12	380	10.9	862	2	US-08-914-520-2
13	380	10.9	862	4	US-09-853-180B-4
14	380	10.9	864	4	US-09-949-016-7758
15	298.5	8.5	783	6	5422248-2
16	298.5	8.5	783	6	5422248-2
17	297.5	8.5	836	1	US-07-923-976-4
18	294.5	8.4	602	2	US-08-419-652-6
19	292	8.3	863	1	US-07-923-976-8
20	277	7.9	837	1	US-07-923-976-2
21	268.5	7.7	771	1	US-07-923-976-6
22	250	7.1	918	4	US-09-853-180B-3
23	248	7.1	708	1	US-07-797-556-2
24	248	7.1	708	1	US-08-308-881-2
25	248	7.1	708	2	US-09-058-263-3
26	248	7.1	708	2	US-09-059-099-2
27	248	7.1	708	3	US-09-058-264-2

28	248	7.1	708	4	US-09-455-962-2	Sequence 2, Appli
29	248	7.1	708	5	PCT-US95-06530-2	Sequence 2, Appli
30	247	7.1	918	2	US-08-825-558-6	Sequence 6, Appli
31	247	7.1	918	3	US-09-312-611-6	Sequence 6, Appli
32	236.5	6.8	572	2	US-08-419-652-5	Sequence 6, Appli
33	226	6.5	979	1	US-08-308-881-6	Sequence 6, Appli
34	226	6.5	979	2	US-09-058-263-6	Sequence 6, Appli
35	226	6.5	979	2	US-09-059-099-6	Sequence 6, Appli
36	226	6.5	979	3	US-09-058-264-6	Sequence 6, Appli
37	226	6.5	979	4	US-09-455-962-6	Sequence 6, Appli
38	226	6.5	979	5	PCT-US95-06530-6	Sequence 6, Appli
39	217.5	6.2	951	4	US-09-313-942-9	Sequence 9, Appli
40	210	6.0	658	2	US-08-825-558-4	Sequence 4, Appli
41	210	6.0	658	3	US-09-312-611-4	Sequence 4, Appli
42	206.5	5.9	1097	1	US-07-943-843-6	Sequence 6, Appli
43	206.5	5.9	1097	1	US-08-347-003-6	Sequence 6, Appli
44	206.5	5.9	1097	4	US-09-949-016-6209	Sequence 6209, Ap
45	206.5	5.9	1119	4	US-09-949-016-10081	Sequence 10081, A

ALIGNMENTS

RESULT 1  
US-08-653-740-5  
; Sequence 5, Application US/08653740  
; Patent No. 5792850  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-653-740-5

Query Match 100.0%; Score 3498; DB 1; Length 636;  
Best Local Similarity 100.0%; Pred. No. 8.1e-280;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGGRGAPFWLPLKALLPLLVLFQRTPOGSAGPLQCYGVGPIGLDNCWEPLGDL 60  
Db 1 MRGGRGAPFWLPLKALLPLLVLFQRTPOGSAGPLQCYGVGPIGLDNCWEPLGDL 60

5,925,735  
6,080,406



;; CITY: Seattle  
;; STATE: WA  
;; COUNTRY: USA  
;; ZIP: 98102  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/275,925  
;; FILING DATE:  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parker, Gary E  
;; REGISTRATION NUMBER: 31,648  
;; REFERENCE/DOCKET NUMBER: 95-31  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 206-442-6673  
;; TELEFAX: 206-442-6678  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 636 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-275-925-5  
;;  
Query Match 100.0%; Score 3498; DB 3; Length 636;  
Best Local Similarity 100.0%; Pred. No. 8.1e-280;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60  
QY 61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVFV 120  
DB 61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVFV 120  
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DB 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
QY 241 NLCGTPGGEPEPLLLWKAAPGCVQVSYKVMFWGGRGLSPGEGITCCCSLIIPSGAEWARVSA 300  
DB 241 NLCGTPGGEPEPLLLWKAAPGCVQVSYKVMFWGGRGLSPGEGITCCCSLIIPSGAEWARVSA 300  
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DB 301 VNATSWPEPLTNLSVCLDSASAPRSVAVSSISAGSTELLVTWQPGPGLSHVVDWARDGD 360  
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DB 361 PLEKLNWVRPPGNLSALLPGNFVGPYRITVTAVSAGLASVYGMVNGTQSVTLPLD 420  
QY 421 TLMRLQDAPCTPAIANGVPRHQRLGHLTHYTLCAQSGTSPSCMVNGTQSVTLPLD 480  
DB 421 TLMRLQDAPCTPAIANGVPRHQRLGHLTHYTLCAQSGTSPSCMVNGTQSVTLPLD 480  
QY 481 PWGCELVWVTASTIAGQPGPIRLHLPLONTLWVKVLPGLIFLWGLFLGCGLSLATSG 540  
DB 481 PWGCELVWVTASTIAGQPGPIRLHLPLONTLWVKVLPGLIFLWGLFLGCGLSLATSG 540  
QY 541 RCYHLRHVKVLPRTWKEVDPDANSSGQPMQVPEAQPLGDLPLILEVEEMEPVWESS 600  
DB 541 RCYHLRHVKVLPRTWKEVDPDANSSGQPMQVPEAQPLGDLPLILEVEEMEPVWESS 600  
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Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636  
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RESULT 4  
US-08-653-740-3  
;; Sequence 3, Application US/08653740  
;; Patent No. 5792850  
;; GENERAL INFORMATION:  
;; APPLICANT: James W. Baumgartner  
;; APPLICANT: Donald C. Foster  
;; APPLICANT: Frank J. Grant  
;; APPLICANT: Cindy A. Sprecher  
;; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
;; NUMBER OF SEQUENCES: 42  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Zymogenetics, Inc.  
;; STREET: 1201 Eastlake Avenue East  
;; CITY: Seattle  
;; STATE: WA  
;; COUNTRY: USA  
;; ZIP: 98102  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/653,740  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parker, Gary E  
;; REGISTRATION NUMBER: 31,648  
;; REFERENCE/DOCKET NUMBER: 95-31  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 206-442-6673  
;; TELEFAX: 206-442-6678  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 578 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-653-740-3

Query Match 90.1%; Score 3150; DB 1; Length 578;  
Best Local Similarity 90.9%; Pred. No. 3.5e-251;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;  
QY 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60  
DB 1 MRGGRGAPFWLWPLPKLALLPLLVLFQRTTRPGSAGPLQCYGVGLDNCSEWPLGDL 60  
QY 61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVFV 120  
DB 61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPPVFV 120  
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180  
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DB 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
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DB 241 NLCGTPGGEPEPLLLWKAAPGCVQVSYKVMFWGGRGLSPGEGITCCCSLIIPSGAEWARVSA 300  
QY 301 VNATSWPEPLTNLSVCLDSASAPRSVAVSSISAGSTELLVTWQPGPGLSHVVDWARDGD 360  
DB 301 VNATSWPEPLTNLSVCLDSASAPRSVAVSSISAGSTELLVTWQPGPGLSHVVDWARDGD 360

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DB 361 PLEKLNWVRLPPGNLSALLPGNFTVGVYRITVTAVASGLASASVWGFREELAPLVGP 420  
QY 421 TLWRLQDAPPGTAPAIWGEVPRHQLRGLHLYTLCAQSGTSPSVCNMVSGNTQSVTLPL 480  
DB 421 TLWRLQDAPPGTAPAIWGEVPRHQLRGLHLYTLCAQSGTSPSVCNMVSGNTQSVTLPL 480  
QY 481 PWGPCBLWWTASTIAGQGGPPGILRLHLPDNTLRWKVLPGLILFLGCLGSLATSG 540  
DB 481 PWGPCBLWWTASTIAGQGGPPGILRLHLPDNTLRWKVLPGLILFLGCLGSLATSG 540  
QY 541 RCYHLRHKVLPWVWEKVPDPANSSSGQHPMEQVPEAQLGDLPLILEVEEMEPVPPVMESS 600  
DB 541 RCYHLRHKVLPWVWEKVPDPANSSSGQHPMEQVPEAQLGDLPLILEVEEMEPVPPVMESS 600  
QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
DB 567 -----GLLGPPRPQVLA 578

## RESULT 5

US-09-073-594-3  
; Sequence 3, Application US/09073594  
; Patent No. 5925735  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,594  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 578 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-073-594-3

Query Match 90.1%; Score 3150; DB 2; Length 578;  
Best Local Similarity 90.9%; Pred. No. 3.5e-251;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

QY 1 MRGGCAPFWLWPLPKALLPLLWVLFQTRPGSAGPLQCYGVGGLDNCWSWELPLGDL 60  
DB 1 MRGGCAPFWLWPLPKALLPLLWVLFQTRPGSAGPLQCYGVGGLDNCWSWELPLGDL 60  
QY 61 GAPSELHLOSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTRAGQPLWPPV 120

DB 61 GAPSELHLOSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTRAGQPLWPPV 120  
QY 121 NLETKMKNAPRLGPDVDVDFSEDDPLEATVHHAPPTWPSHKVLI COFYHRRCOEAAWTLLE 180  
DB 121 NLETKMKNAPRLGPDVDVDFSEDDPLEATVHHAPPTWPSHKVLI COFYHRRCOEAAWTLLE 180  
QY 181 PELKTIPLTPTVEIQLELATGVKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
DB 181 PELKTIPLTPTVEIQLELATGVKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
QY 241 NLGCTPGGEEPLLWKAPGCPQVSYKYVFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300  
DB 241 NLGCTPGGEEPLLWKAPGCPQVSYKYVFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300  
QY 301 VNATSWELTNLSVCLDSASAPRSVAVSSIAGSTELLVTPQGPGEPLHVVWDWARDGD 360  
DB 301 VNATSWELTNLSVCLDSASAPRSVAVSSIAGSTELLVTPQGPGEPLHVVWDWARDGD 360  
QY 361 PLEKLNWVRLPPGNLSALLPGNFTVGVYRITVTAVASGLASASVWGFREELAPLVGP 420  
DB 361 PLEKLNWVRLPPGNLSALLPGNFTVGVYRITVTAVASGLASASVWGFREELAPLVGP 420  
QY 421 TLWRLQDAPPGTAPAIWGEVPRHQLRGLHLYTLCAQSGTSPSVCNMVSGNTQSVTLPL 480  
DB 421 TLWRLQDAPPGTAPAIWGEVPRHQLRGLHLYTLCAQSGTSPSVCNMVSGNTQSVTLPL 480  
QY 481 PWGPCBLWWTASTIAGQGGPPGILRLHLPDNTLRWKVLPGLILFLGCLGSLATSG 540  
DB 481 PWGPCBLWWTASTIAGQGGPPGILRLHLPDNTLRWKVLPGLILFLGCLGSLATSG 540  
QY 541 RCYHLRHKVLPWVWEKVPDPANSSSGQHPMEQVPEAQLGDLPLILEVEEMEPVPPVMESS 600  
DB 541 RCYHLRHKVLPWVWEKVPDPANSSSGQHPMEQVPEAQLGDLPLILEVEEMEPVPPVMESS 600  
QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
DB 567 -----GLLGPPRPQVLA 578

## RESULT 6

US-09-275-925-3  
; Sequence 3, Application US/09275925  
; Patent No. 6080406  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/275,925  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673

```

; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-275-925-3

Query Match          90.1%; Score 3150; DB 3; Length 578;
Best Local Similarity 90.9%; Pred. No. 3.5e-251;
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

Qy 1 MRGRGAPFWMPLPKLALLPLLVLFQRTTRPQSGAGPLQCYGVGPGDLNCSWEPLGDL 60
Db 1 MRGRGAPFWMPLPKLALLPLLVLFQRTTRPQSGAGPLQCYGVGPGDLNCSWEPLGDL 60
Qy 61 GAPSELHLOKQYRSNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPFV 120
Db 61 GAPSELHLOKQYRSNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPFV 120
Qy 121 NLETKMPNAPRLGPDVDFSDDDPLEATVHWAPPTWPSHKVLCOPHYRCQEAATLLE 180
Db 121 NLETKMPNAPRLGPDVDFSDDDPLEATVHWAPPTWPSHKVLCOPHYRCQEAATLLE 180
Qy 181 PELKTIPLTPVEIQDELATGYKYVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Db 181 PELKTIPLTPVEIQDELATGYKYVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSG 240
Qy 241 NLCGTPGGEPLLLWKAPGCVQVYKWFVWVGRELSPEGITCCCSLIIPSGAEWAVRSA 300
Db 241 NLCGTPGGEPLLLWKAPGCVQVYKWFVWVGRELSPEGITCCCSLIIPSGAEWAVRSA 300
Qy 301 VNATSWPEPLNLSLVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLSHVVDWARDGD 360
Db 301 VNATSWPEPLNLSLVCLDSASAPRSVAVSSTAGSTELLVTWQPGPGLSHVVDWARDGD 360
Qy 361 PLEKLNVRPLPPGNLSALLPGNFVTPYRITVAVSASGLASASSVWGFREELAPLVGP 420
Db 361 PLEKLNVRPLPPGNLSALLPGNFVTPYRITVAVSASGLASASSVWGFREELAPLVGP 420
Qy 421 TLWLQDAPGTPAIANGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSNGTQSVTLPLDL 480
Db 421 TLWLQDAPGTPAIANGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSNGTQSVTLPLDL 480
Qy 481 PWGCELVWVTAATAGGPGPILRLHLPNTLRKVLPGILFLWGLFLGCGLSLATSG 540
Db 481 PWGCELVWVTAATAGGPGPILRLHLPNTLRKVLPGILFLWGLFLGCGLSLATSG 540
Qy 541 RCYHLRHKVLPWWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVVMSS 600
Db 541 RCYHLRHKVLPWWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVVMSS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 567 -----GLLGPPRPQVLA 578

RESULT 7
US-08-653-740-7
; Sequence 7, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42.
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle

```

```

; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,740
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-740-7

Query Match          58.4%; Score 2044; DB 1; Length 623;
Best Local Similarity 62.8%; Pred. No. 6.3e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 14 LPKLALLPLLVLFQRTTRPQSGAGPLQCYGVGPGDLNCSWEPLGDLGAPSELHLOKQY 73
Db 9 LTPLELLLSLMSLLGTRPHGSPGLQCYSGVGLILNCSWEPLGDLTETPVLVHQOKY 68
Qy 74 RSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLWPFVFNLTQMKPNAPRL 133
Db 69 HPNRVWEKVPKQSWVTIPREQLTMSDKLLVWGTAKGQPLWGSVSVNLTQMKPDPQI 128
Qy 134 GPVDVSEDDPLEATVHWAPPTWPSHKVLCOPHYRCQEAATLLEPELKTIPLTVEI 193
Db 129 FSQVDISEATLSEATLQVWAPPVPPQKALTQCPRYKECQAEATRLPEQLKLTPEVEM 188
Qy 194 QDELATGYKYVGRCRMEKEEDLWGEWSPILSFOTPPSAPKDVWVSNLCTGPGEBPL 253
Db 189 QNLEPGTCQVSRCCQVENGYP-WGEWSPILSFOTPFDPEDVWVGTVCTSGKRAALL 247
Qy 254 LKAPGPCVQVSYKWFVWVGRELSPEGITCCCSLIIPSGAEWAVRSVAVNATSWPEPLNLS 313
Db 248 VMKDPKPCQVTVYVWFGAGDITTTQBEVPCCKSPVPANMEWAVSPGNSTSWVPPTNLS 307
Qy 314 LVCLDSASAPRSVAVSISAGSTELLVTWQPGCEPLEHVVVDWARDGDPLEKLNVRPLPG 373
Db 308 LVCLAPESAPCDVGVSSADGSPGIVTKQGTAKPLEYVYVVDWAQDGLDKLWNLRLPPG 367
Qy 374 NLSALLPGNFTVGPYRITVAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPGTP 433
Db 368 NLSTLLPGFEGKGVPIRITVAVYSGLAHAPSVMGFREELVPLAGPWNRLDDPDPGTP 427
Qy 434 ATANGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSNGTQSVTLPLDLPWGPCELWVTAST 493
Db 428 VWANGEVPRHQLRGLHTHYTCISQSGRLSTVCRNVSSQTQTATLPLNLSHSGFSLWVTST 487
Qy 494 IAGQGGPGLRLHLPNTLRKVLPGILFLWGLFLGCGLSLATSG-----GRCYHLRHKV 549
Db 488 VAGQGGPGLDLSLHLPDNRIRKWLFWFLSLWGLLWGLGCGLSLATSTRCLQARCLHWRHKL 547
Qy 550 LPEWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVPMWESSQPAQATPL 609
Db 548 LPQWIWVRVDPANSSSQPHMEQVPEAQPLGDLPILEVEELPQPKDGPILVEVEELPQPVES 604
Qy 610 DSGYEKHFLLPTPEELGLL 627

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Db      605 YSGYKHFLLPTPEELGLL 622

RESULT 8
US-09-073-594-7
; Sequence 7, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6678
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-594-7

Query Match      58.4%; Score 2044; DB 2; Length 623;
Best Local Similarity 62.8%; Pred. No. 6.3e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy      14 LPKALLPWLFWLFTQTRPGSAGPLQCYGVGPLGLNCSWEPLDGLGAPSELHLQSKY 73
Db      9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLDGLTTPVLYHQSKY 68

Qy      74 RSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFVNLETQMKPNAPRL 133
Db      69 HNRVWEVKVPSKSVVTIPREQFTWADKLLIWGTQKGRPLMSSVSVNLETQMKDPTQI 128

Qy      134 GPDVDFSEDDPLEATHVWAPPPTWPSHKVLCQHYRRCQEAATWILLEPELKIPIPTPVEI 193
Db      129 FSQVDISEATEATVQNAAPPVPPWPPKALTQFRYKECAQEAATWLEPQLKTDGLTPVEM 188

Qy      194 QDELATGKAVGRCRMEKEEDLWGSWSPILSFQTPPSAPKDVWVSGNLCGTPGGEPLL 253
Db      189 QNLEPCTCQVSGRCQVENGYP-WGWSWSPILSFQTPFLDPEDVWVSGTVCETSGKRAALL 247

Qy      254 LMKAGPCVQVSKYKWFVWGGRELSPEGITCCCLIPSGAEARWASVAVNATSWPEPLTNLS 313
Db      248 WVKDPRPCQVTVTVWFGADITTTQEEVPCCKSPVPAMWENAVVSPGNSTSWVPPTNLS 307

Qy      314 LVCLDSASAPRSVAVSSIGSTELLITWQFGGEPLEHVVDWARDGDDPLEKLNWRLPPG 373
Db      308 LVCLAPESAPCDVGVSSADSGSPGIKVTVWQGRKPLEYVVDWAQDGDSDKLNWRLPPG 367

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RESULT 9
US-09-275-925-7
; Sequence 7, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6678
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-275-925-7

Query Match      58.4%; Score 2044; DB 3; Length 623;
Best Local Similarity 62.8%; Pred. No. 6.3e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy      14 LPKALLPWLFWLFTQTRPGSAGPLQCYGVGPLGLNCSWEPLDGLGAPSELHLQSKY 73
Db      9 LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLDGLTTPVLYHQSKY 68

Qy      74 RSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFVNLETQMKPNAPRL 133

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Db 69 HPNRVWVUPSKQSWTTPREQFTMADKLLIWTQKGRPLMSVSVNLETKQMKDTPQI 128  
Qy 134 GPDVDFEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATWLLPELKTIPLEVEI 193  
Db 129 FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKCEQAEATWRLPQLKTDGLITVEM 188  
Qy 194 QDLELATGYKYGRCKMEEDLWGEWSPILSFOTPPSAKDVVWVSGNLCTGPGGEBPLL 253  
Db 189 QNLEPGTCYQVSGRCQVGYGYP-WGEWSSPLSFOTPFDPEDVWVSGTVCETSGKRAALL 247  
Qy 254 LKAPGFCVQVSYKVFVWVSGRELSPGIGTCCCSLIPSGAEWARVSAVNTWEPNLNLS 313  
Db 248 VKMDPRCVQVYTYVWFGAGDITTTQEEVPCCKSPVFWMEWAVVSPGNSTSWVPPTNLS 307  
Qy 314 LVCLDSASAPRSVAVSSIAGSTELLVWQPGGEPLEHVVDWARDGDPLEKLNWRLPPG 373  
Db 308 LVCLAPESAPCDVGSADSGPGIKVTKQGRKPLEYVVDWQAQDGLSKLNWRLPPG 367  
Qy 374 NLSALLPGNTVGVYPRITVAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPPGTP 433  
Db 368 NLSTLLPGEPKGGVYPRITVAVSASGLAAPSVMGFREELVPLAGPAVWRLPDDPPGTP 427  
Qy 434 AIWGEVPRHQLRHLTHYTLCAQSGTSPSVMVNGTQSVTLPLDLPWGPCELWYAST 493  
Db 428 VWAGEVPRHQLRQATHTYTCIQSRLSTVCRNVSSQTQTATLNLHSGFKLWYTVST 487  
Qy 494 IAGQPGPTLRLHLPNTLRLWKLPGILFLWGLFLGCGLSLATS---GRCVHLRHKV 549  
Db 488 VAGQPGPDLSLHPDNRIRWALPWFSLWGLLWGLGCGLSLATSCLQARCLWHLK 547  
Qy 550 LPRWVWKVPPDANSQSGPHMEQVPEAQPLGDLPILEVEEMPPVWESSQPAQATAPL 609  
Db 548 LPQWIERVDPDANSQSGPYKEVSLPQPPKDGPILEVEEVELQPVVES---PKASAPI 604  
Qy 610 DSGYKHFLLTPBELGLL 627  
Db 605 YSGYKHFLLTPBELGLL 622

## RESULT 10

US-08-685-118-2

; Sequence 2, Application US/08685118

; Patent No. 5840530

; GENERAL INFORMATION:

; APPLICANT: Gubler, Ulrich A

; APPLICANT: Presky, David H

; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann-La Roche Inc.

; STREET: 340 Kingsland Street

; CITY: Nutley

; STATE: NJ

; COUNTRY: USA

; ZIP: 07110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/685,118

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Silverman, Robert A.

; REGISTRATION NUMBER: 35,682

; REFERENCE/DOCKET NUMBER: CD 9195

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201) 235-2863

; TELEFAX: (201) 235-2363

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 862 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-685-118-2

Query Match 10.9%; Score 380; DB 2; Length 862;

Best Local Similarity 25.3%; Pred. No. 1.7e-22;

Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Qy 31 RPOGSAGPLQCYGVPLGDLNCSWEPLGD-----LGAPSEHLHLSQ----- 71

Db 126 QPQN-----LSCIOKSGQVACTWGRDTHLYTEYTLQSGPKNLWQCKDIYCDYL 181

Qy 72 -----KYRNKTKTV-AVAGRSWVAIPREQLTMSDKLLVWGTKAGQPLPMPFVN 121

Db 182 DFGINLTSPESPENFTAKVTAVNSLSSSLP-STETFLDIV-----RPL-PPWDIR 231

Qy 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATWLLPE 181

Db 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYRPSNLSLNN--- 269

Qy 182 ELXTIPLTPV-----ETDLELATGYKYVGRCKMEEDLWGEWSPILSFOTP---PSAPK 234

Db 270 ----VNVTKAKGRHDLDDLPFTFEYEFQISSKLHYKGSWDSSELSRAQTPBEEPTGML 325

Qy 235 DVWVSGNLCTPGGEBPLLLWK-----APGPCVQVSYKVFVWVWGGRELSP---GITCCC 286

Db 326 DVWYKGRHDIY-SRQISLSFWKLSVSEARGKILHYQVTLQELTGKAMTONITGHTSWT 384

Qy 287 SLTPSGAEMA-RVSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSIAGSTELLVWQP 343

Db 385 TVIPRTGNWAVAVSAANSKSGSLPTRINIMNLCEAGLLAPROVSANS-EGMDNLTWQP 443

Qy 344 ---GPGEPLEHVVDWAR---DGDPLEKLNWRLPQNLSSALLPCNFTVGVYPRITVAVS 397

Db 444 PRKDPASVQEVYVWEMRELHPGGDTQVPLNWRSPYNVSALISENISKYCYEIRVYALS 503

Qy 398 ASGLASASSVWGFREELAPLVGPTLWRLQDAPGTPAIWGEVPRHQLRHLTHYTLCA-- 455

Db 504 GD-QGCGSSILGNSKHKAPLSGPHINAIT-EGKSILISWNSIPVQEQMGLLHYRIYWK 561

Qy 456 -AQSGTSPSYC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQPPGPIRLHLDPN 511

Db 562 ERDSNSQPQLCEIPYRVSONSHPIINSIQ-PRVTYVLMWMTALTAAGSSHGNEREFCL-QG 619

Qy 512 TLRWK-VLPGI---LFLWGLFLLGCGLSLATSGRCVHLRHKVL-----PRWVWKVP 559

Db 620 KANWMAFVAPSICIAIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667

Qy 560 DPANSSSGQPH-----MEQVPEAQPLGDLPILEVEEMPPVWESSQPAQATA-----PLD 610

Db 668 DPANSTCAKKYPIAEKTLQPLDRLLDWPTP-----DPELVISEVLHQTVPVFRHPPC 723

Qy 611 SGYKHFLLTPBELGLL-----PPRPQVL 635

Db 724 SNWPQ-----REKGIQGHQASEKMMHSSSPPPRAL 756

## RESULT 11

US-08-915-495-2

; Sequence 2, Application US/08915495

; Patent No. 5852176

; GENERAL INFORMATION:

; APPLICANT: Gubler, Ulrich A

; APPLICANT: Presky, David H

; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann-La Roche Inc.

; STREET: 340 Kingsland Street

; CITY: Nutley

; STATE: NJ



```

; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,495
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-915-495-2

Query Match 10.9%; Score 380; DB 2; Length 862;
Best Local Similarity 25.3%; Pred. No. 1.7e-22;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPLQCVGVGPGDLNCSWEPLGD-----LGAPSEHLHLSQ----- 71
DB 126 QPQN-----LSCIQGEGQVACTWGERDTHLYTEYTLQSLGPKNLTWQCKQKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAGRSWVAIPREOLTMSDKLLVMGTRKAGQPLWPPVFN 121
DB 182 DFGINLTPEPSNFATAKVTAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLCQPHYRCQBAATWLLPE 181
DB 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYRPSNRLNWM--- 269
QY 182 ELKTIPLTPV-----EIQDLELATGYKVGRCRMEKEEDLWGEWSPILSFQTP---PSAPK 234
DB 270 -----VNVTKAKGRHDLDLKPFTEYEFQISSKLHLYKGSWSDWSESLRAQTPPEEPTGML 325
QY 235 DVWVSGNLCTPGGEPILLWK-----APGFCVQVSYKVFVWVGRELSPE--GITCCC 286
DB 326 DVWYMKRHIDY-SRQGISLFWNLSVSEARGKILHYQVTLQELTGKANTQNIHTSWT 384
QY 287 SLIPSGAEWA-RVSAVNA--TSWEPLTNLSVLCLDSAGAPRSVAVSSIAGSTELLVWQP 343
DB 385 TVIPRTGNWAVSAANSKGSLLPTRINIMNLCEAGLLAPROVANS-EGMDNLTWQP 443
QY 344 ---GPCEPLEHVVDWAR---DGDPLEKLNWPLPGNLSALLPGNFTVGPVRIYTVAVS 397
DB 444 PRKDPASVQVEYVREHLPGGDTQVPLNLSRFPVNSALISENIKSYICYEIRVYALS 503
QY 398 ASGLASASVWGPRELAPLVGPTLWRLQDAPGTPATAWGVPRHQLRGHLTHYTLG-- 455
DB 504 GD-QGGCSILGNSKHKAPLSGFHNAITE-EKGSILISWNSIPVQEQMGCLLHRYIWK 561
QY 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDPLMGWPCBLWVTASTIAGQPPGPIRLHLDPN 511
DB 562 ERDSNSQPQLCBIPYRVSNQSHPINSLQ-PRVTYVLLWMTALTAAAGSSHGNERFCL-QG 619
QY 512 TLRWK--VLPGL---LFLWGLFLGGLSLATSGRYHLRHVKV-----PRWVWEKVP 559
DB 620 KANWMAFAPSICIAIIMVGIF-----STHYFQQKVFVLLAALRPQWCSEIRP 667

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QY 560 DPANSSGQPH-----MEQVPEAOPLGDLPILEVEEMEPVPPVMESSQPAQATA-----PLD 610
DB 668 DPANSTCAKYPVIAEKEKTLQPLDRLLDWPTPE-----DPEPLVISEVLHQLVTPVFRHPPC 723
QY 611 SGYKHFILPTPEELGLLG-----PPRPQVL 635
DB 724 SNWPQ-----REKGIQGHQASEKDMHMSASSPPPPRAL 756

RESULT 12
US-08-914-520-2
; Sequence 2, Application US/08914520
; Patent No. 5919903
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A.
; APPLICANT: Presky, David H.
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,520
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-914-520-2

Query Match 10.9%; Score 380; DB 2; Length 862;
Best Local Similarity 25.3%; Pred. No. 1.7e-22;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPLQCVGVGPGDLNCSWEPLGD-----LGAPSEHLHLSQ----- 71
DB 126 QPQN-----LSCIQGEGQVACTWGERDTHLYTEYTLQSLGPKNLTWQCKQKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAGRSWVAIPREOLTMSDKLLVMGTRKAGQPLWPPVFN 121
DB 182 DFGINLTPEPSNFATAKVTAVNSLGSSSSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLCQPHYRCQBAATWLLPE 181
DB 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYRPSNRLNWM--- 269
QY 182 ELKTIPLTPV-----EIQDLELATGYKVGRCRMEKEEDLWGEWSPILSFQTP---PSAPK 234
DB 270 -----VNVTKAKGRHDLDLKPFTEYEFQISSKLHLYKGSWSDWSESLRAQTPPEEPTGML 325
QY 235 DVWVSGNLCTPGGEPILLWK-----APGFCVQVSYKVFVWVGRELSPE--GITCCC 286

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Db 326 DVWTKRHIDY-SRQQLSLFWKNSVSEARGKILHYQVTLQELTGGKAMTQNIHTGTSWT 384  
Qy 287 SLIPSGAWEA-RVSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSITAGSTELLVTWQP 343  
Db 385 TVIPRTGNWAVAVSAANSKSSLPTRINIMNLCAGLLAPQVSANS-EGMDNLTVTWQP 443  
Qy 344 ---GPGPLEHVVDWAR---DGDPLEKLNWRLPPGNLSALLPQNTFTVGVYRITVTAVS 397  
Db 444 PRKDPASVQVYVWEVRELHPGGDTQVPLNWLRSRPNVNSALISENISKYICYEIRVVALS 503  
Qy 398 ASGLASASSVWGPREELAPLVGPTLWRLQDAPPTGPAIAMEGEVPRHQLRHLTHYTL-- 455  
Db 504 GD-QGGCSSILGNSKHPALSGPHINAITE-EKGSILISWNSIPVQSGMGLLHYRIYWK 561  
Qy 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQPPGPIRLHLHPDN 511  
Db 562 ERDSNSQPOLCEIPIRVSONSHPINSLQ-PRVTYVLMWLTALTAAGSSHGNREFCL-QG 619  
Qy 512 TLRWK--VLPQI---LFLWGLFLGCGLSLATSRCVHLRHVVL-----PRWWEKVP 559  
Db 620 KANWMAFVAPSIICIAIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667  
Qy 560 DPANSSSQPH---MEQVPEAQPLGDLPILEVEEMEPVPMWESSQPAQATA---PLD 610  
Db 668 DPANSTCAKYPPIAEKTLQPLDLRLIDWPTPE---DPEPLVISEVHLVQVTPVFRHPPC 723  
Qy 611 SGYEKHLPTPEELGLLG-----PPRQVLT 635  
Db 724 SNWPQ-----REKGIQHQASEKMDMHSASSPPPPRAL 756

## RESULT 13

US-09-853-180B-4  
; Sequence 4, Application US/09853180B  
; Patent No. 6756481  
; GENERAL INFORMATION:  
; APPLICANT: Chirica, Madaline  
; APPLICANT: Parham, Christi L.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Moore, Kevin W.  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
; FILE REFERENCE: DX01074  
; CURRENT APPLICATION NUMBER: US/09/853,180B  
; PRIOR FILING DATE: 2001-05-10  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 4  
; LENGTH: 862  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-180B-4

Query Match 10.9%; Score 380; DB 4; Length 862;  
Best Local Similarity 25.3%; Pred. No. 1.7e-22;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;  
Qy 31 RPOGSAGPLOCYGVGPGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71  
Db 126 QPQN---LSCIQKGEQGTACTWGERDTHLYTEYTLQSLGPKNLTWQCKDIYCDYL 181  
Qy 72 -----KYRSNKTQTV-AVAGRSWVAIPREQLTMSDKLLVWGTKACQPLWPPVFN 121  
Db 182 DFGINLTPESPESNFTAKVTAVNSLSSSSLP-STFTFLDIV-----RPL-PPWDIR 231  
Qy 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLIQCFHYRRQCEAAWLTLEP 181  
Db 232 IKFO-KASVSR-----CTLYWR-----DGLVLLNKLRLRPSNRLWN--- 269  
Qy 182 ELKTIPLTPV---EIQDLELATQYKVGCRMEKEEDLWGEWSPILSFQTP---PSAPK 234

Db 270 ----VNVTKAKGRHDLDLKPFTEYEFQISSKHLHYKGSWDSSESURAOPTPEEPTGML 325  
Qy 235 DVWVSGNLCTPGGEEPLLLWK-----APGPCVQVSYKVMFWYGGRELSP--GITCCC 286  
Db 326 DVWTKRHIDY-SRQQLSLFWKNSVSEARGKILHYQVTLQELTGGKAMTQNIHTGTSWT 384  
Qy 287 SLIPSGAWEA-RVSAVNA--TSWEPLTNLSLVCLDSASAPRSVAVSSITAGSTELLVTWQP 343  
Db 385 TVIPRTGNWAVAVSAANSKSSLPTRINIMNLCAGLLAPQVSANS-EGMDNLTVTWQP 443  
Qy 344 ---GPGPLEHVVDWAR---DGDPLEKLNWRLPPGNLSALLPQNTFTVGVYRITVTAVS 397  
Db 444 PRKDPASVQVYVWEVRELHPGGDTQVPLNWLRSRPNVNSALISENISKYICYEIRVVALS 503  
Qy 398 ASGLASASSVWGPREELAPLVGPTLWRLQDAPPTGPAIAMEGEVPRHQLRHLTHYTL-- 455  
Db 504 GD-QGGCSSILGNSKHPALSGPHINAITE-EKGSILISWNSIPVQSGMGLLHYRIYWK 561  
Qy 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGQPPGPIRLHLHPDN 511  
Db 562 ERDSNSQPOLCEIPIRVSONSHPINSLQ-PRVTYVLMWLTALTAAGSSHGNREFCL-QG 619  
Qy 512 TLRWK--VLPQI---LFLWGLFLGCGLSLATSRCVHLRHVVL-----PRWWEKVP 559  
Db 620 KANWMAFVAPSIICIAIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667  
Qy 560 DPANSSSQPH---MEQVPEAQPLGDLPILEVEEMEPVPMWESSQPAQATA---PLD 610  
Db 668 DPANSTCAKYPPIAEKTLQPLDLRLIDWPTPE---DPEPLVISEVHLVQVTPVFRHPPC 723  
Qy 611 SGYEKHLPTPEELGLLG-----PPRQVLT 635  
Db 724 SNWPQ-----REKGIQHQASEKMDMHSASSPPPPRAL 756

## RESULT 14

US-09-949-016-7758  
; Sequence 7758, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7758  
; LENGTH: 864  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7758

Query Match 10.9%; Score 380; DB 4; Length 864;  
Best Local Similarity 25.3%; Pred. No. 1.7e-22;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;  
Qy 31 RPOGSAGPLOCYGVGPGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71  
Db 128 QPQN---LSCIQKGEQGTACTWGERDTHLYTEYTLQSLGPKNLTWQCKDIYCDYL 183  
Qy 72 -----KYRSNKTQTV-AVAGRSWVAIPREQLTMSDKLLVWGTKACQPLWPPVFN 121  
Db 184 DFGINLTPESPESNFTAKVTAVNSLSSSSLP-STFTFLDIV-----RPL-PPWDIR 233  
Qy 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLIQCFHYRRQCEAAWLTLEP 181

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Db 234 IKFO-KASVSR-----CTLYR-----DEGLVLLNRLRYRPSNRLWNM--- 271
QY 182 ELKTIPLTPV-----ETODLELATGYVGRCRMKEEDLWGSWSPILSFQTP--PSAPK 234
Db 272 ----VNVTKAKGRHLLDLKPTEYFQISSKHLHYKGSWSWDSLSRAQTPEEPTGML 327
QY 235 DVWVSGNLCTPGGEPILLWK-----APGPCVQVSVKVFVWVGRELSPB--GITCC 286
Db 328 DWVYKRDYD-SRQOISLFWKNLSVSEARGKILHYQVTLQBLTGKANTQITGHTSWT 386
QY 287 SLIPSGAWA-RVSAVNA--TSWEPLTNLSVCLDSASAPRSVAVSSIAGSTELLVTWQP 343
Db 387 TVIPRTGNWAVASANSKSSLPTRINIMNLCEAGLLAPROVSANS--EGMDNILVTWQP 445
QY 344 ---GPCEPLEHVVDWAR---DGDPLEKLNWRLPQGNLSALLPGNFTVGPVRYITVAVS 397
Db 446 PRKDPASVQEVYVWRELPHGGDTQVPLNWLRSRPNVSALISENKSICYEIRVYALS 505
QY 398 ASGLASASVWGFREELAPLVGPTLWRLQDAPGTPAIAGVPRHOLRGHLTHVTLG-- 455
Db 506 GD-QGCSILGNKHKALSGPHINAITE-EKGSILISWNSIPVQEQMGCLLHYRYWK 563
QY 456 -AQSGTSPVC---MNVSGNTQSVTLPLDLPWGPCELWVTASTIAGOGPPGPIRLHLDPN 511
Db 564 ERDSNSQPCLCEIPYRVSONSHPIINSIQ-PRVTYVLMWTALTAAGESSHGNREFCL-QG 621
QY 512 TLRWK--VLPGI---LFLWGLFLGCLSLATSGRCYHLRHVKUL-----PRWWEKVP 559
Db 622 KANWAFVAPSICIAIMVIGIF-----STHYFQKQVFLVLLAALRPQWCSEIP 669
QY 560 DPANSSSGOPH-----MEQVPEAQPLGDLPILEVEEMEPWPWESSQPAQATA----PLD 610
Db 670 DPANSTCAKYPAAEKTQPLDRLLIDWPTB-----DPELVISEVLHQVTPVFRHPPC 725
QY 611 SGYERHFLPTPEELGLLG-----PPRPQVL 635
Db 726 SNWPQ-----REKGIQGHQASEKMMHSSASPPPPRAL 758

RESULT 15
5422248-2
;PATENT NO. 5422248
;APPLICANT: SMITH, CRAIG A.;LARSEN, ALF D.;SIMS, JOHN E.;
;BENSON, CURTIS M.
;TITLE OF INVENTION: DNA SEQUENCES ENCODING GRANULOCYTE-COLONY
;STIMULATING FACTOR RECEPTORS
;NUMBER OF SEQUENCES: 6
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/6,183
;FILING DATE: 15-JAN-1993
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 587,329
;FILING DATE: 24-SEP-1990
;APPLICATION NUMBER: 522,952
;FILING DATE: 03-APR-1990
;APPLICATION NUMBER: 416,306
;FILING DATE: 03-OCT-1989
;APPLICATION NUMBER: 412,816
;FILING DATE: 26-SEP-1989
;SEQ ID NO:2
;LENGTH: 783
5422248-2
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Query Match      8.5%; Score 298.5; DB 6; Length 783;
Best Local Similarity 23.5%; Pred. No. 7.8e-16;
Matches 164; Conservative 77; Mismatches 259; Indels 197; Gaps 34;

QY 50 LNCSEPLDGLGAPSELHQSKYRSN-KTQTVAV-----AAGRSWVAIPRELQWSDKL 103
Db 140 LICQEPGPEETHLFTSLFKSFRGNCTQGDSDLDVCPKQDQGHCCIPRKHLLLYQNM 199
QY 104 LVW-----GKAGQPLM-----PPVFVNLETQMKFNAPRLG-----PDVDF 139
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Db 200 GIWQAEALGTSMSPQLCLDPMVVKLEPPMLRTMDSPPEAAPQAGCLOLCMEP---- 255
QY 140 SEDDPLEATVWAPTWPSHKVILCOF-HYRRCOEAAWTLLEPELKTITPLTPVEIQDLEL 198
Db 256 -----WQPLGHINQK---CELHKPQGEASWALVGP-----LPLEALQVEL 294
QY 199 -----ATGYKVVGRCRMEKEEDLWGEWSPILSFOTPPSAPK---DVWVSGNLCTPGGEE 250
Db 295 CGLLPATAYTQIRWPLPQHWSDNSPSLELRTTERAPTIVRLDTPWRQRL-----D 348
QY 251 P---LLLKAPCPQVSVKVMFWVGGRELSPEGITCCSLIPSGAEWARVAVNATSWE 307
Db 349 PRTVQLFWK-FVPLEEDSGRIQGVV-----VSWRPSQAGAILPLCNTTELS 394
QY 308 PLTNL-----SLVCLDSA--SAPRSVAVSSIAGST-----ELLVTWQPGP 346
Db 395 CTFHLPSBAQEAVALVAYNSAGTSRPTPVVFSRGPALTRLHAMARDPHSLWVGWEPNP 454
QY 347 EPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGVRYITVTVASAGLAS 403
Db 455 WPGVVIWGLGPPSASNSKTWMEQNGRATGFLLENIRPFQLYEIIIVTPLYQDTWGP 514
QY 404 ASSVMGFREELAPLVGPTLWRLQDAPGTPAIAGVEPRHOLRGHLTHYTLCAQSGTSPS 463
Db 515 SQHVYVAYSQEMAPSHAPEL-HLKHHIGKTAQLEWVPEPELKGKSPLTHTYTFWNTAQNS 573
QY 464 VCMNVSGNTQSVTLPLDLPWGPCELW-----VTASTIAGOGPPGPIRL 506
Db 574 FSAILNASSRGGFVLHGLE--FASLYHHLMAASQAGATNSTVLTMLTLPES-----EL 626
QY 507 HLPDNTLRWKVLPGLIFLWGLFL--CCGLSLATSGRCYHLRHVKVLPWVWEKVPDPAN 563
Db 627 HI-----ILGFLGILLLLTCLCG---TAWLCCSPNRK---NPLWPSVPDPAH 667
QY 564 SSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEPWP----- 595
Db 668 SSLGSWVPTIMEEDAFQPLGLGTPITKLTVLEDEKFPVWESHNSSETCGLPTLVQTY 727
QY 596 VMESQPAQATAP-LDSGYEXHFLPTPEELGLLGP 631
Db 728 VLQGDPRAVSTQPOSQSG-----TSDQ---AGPPR 754
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Search completed: February 19, 2005, 01:17:41  
Job time : 48 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2005, 01:03:05 ; Search time 175 Seconds  
(without alignments)  
1405.598 Million cell updates/sec

Title: US-10-088-950A-1  
Perfect score: 3498  
Sequence: 1 MRGRGAPFWLWFLKALL.....FLTPBELGLLGP RPQVLA 636

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 AAW33399	Aaw33399 Alternati
2	3498	100.0	636	4 AAG65270	Aag65270 Cell fact
3	3498	100.0	636	4 AAU01853	Aau01853 Human typ
4	3498	100.0	636	7 ADD68151	Add68151 Human WSX
5	3498	100.0	636	7 ADL26574	Adl26574 Human WSX
6	3498	100.0	636	8 ADL91801	Adl91801 Human PRO
7	3498	100.0	636	8 ADL14163	Adl14163 Human NF-
8	3494	99.9	636	5 AEG32294	Abg32294 Human IL-
9	3494	99.9	636	6 ABU09752	Abu09752 Human T-c
10	3494	99.9	636	6 ABG75880	Abg75880 Human int
11	3490	99.8	636	2 AAY23781	Aay23781 Human DNA
12	3316	94.8	604	4 AAG65271	Aag65271 Cell fact
13	3288	94.0	680	6 ABR41219	Abr41219 Human DIT
14	3150	90.1	578	2 AAW33398	Aaw33398 Human hae
15	3007	86.0	558	8 ADO26826	Ado26826 Human rec
16	2875	82.2	523	2 AAY23785	Aay23785 Partial h
17	2044	58.4	623	2 AAW33400	Aaw33400 Mouse hae
18	2044	58.4	623	4 AAU01854	Aau01854 Mouse typ
19	886.5	25.3	246	2 AAY23786	Aay23786 Partial m
20	415	11.9	82	8 ADR20046	Adr20046 Human imm
21	412	11.8	77	7 ADB36344	Adb36344 Human imm
22	400	11.4	150	2 AAY23782	Aay23782 Human DNA
23	380	10.9	862	2 AAW12771	Aaw12771 Human int
24	380	10.9	862	7 ADE33704	Ade33704 Human int
25	380	10.9	862	7 ADF76395	Adf76395 Novel hum

26	380	10.9	862	8 ADK90609	Adk90609 Human IL-
27	380	10.9	862	8 ADM33832	Adm33832 Human IL-
28	380	10.9	862	8 ADO19580	Ado19580 Human PRO
29	380	10.9	862	8 ADP54649	Adp54649 Human PRO
30	331	9.5	861	5 ABB78097	Abb78097 Amino aci
31	330	9.4	861	5 ABB78098	Abb78098 Amino aci
32	298.5	8.5	783	2 AAR11741	Aar11741 Granulocy
33	298.5	8.5	783	2 AAR77868	Aar77868 Human gra
34	298.5	8.5	783	2 AAW10485	Aaw10485 Human gra
35	297.5	8.5	800	2 AAW10486	Aaw10486 Human gra
36	297.5	8.5	801	2 AAR11742	Aar11742 Clone 25-
37	297.5	8.5	813	3 AAB03873	Aab03873 Human gra
38	297.5	8.5	836	2 AAR14255	Aar14255 Human GCS
39	297.5	8.5	836	6 ABU89749	Abu89749 Protein d
40	297.5	8.5	836	8 ADP12979	Adp12979 Protein e
41	297.5	8.5	836	8 ADP44071	Adp44071 Human GCS
42	297.5	8.5	836	8 ADQ59672	Adq59672 Human GCS
43	297.5	8.5	836	8 ADQ60159	Adq60159 Human gra
44	297.5	8.5	836	8 ABM80066	Abm80066 Tumour-as
45	297.5	8.5	836	8 ADP23580	Adp23580 PRO poly

ALIGNMENTS

RESULT 1  
AAW33399  
ID AAW33399 standard; protein; 636 AA.  
XX  
AC AAW33399;  
XX  
DT 22-MAY-1998 (first entry)  
XX  
DE Alternately spliced Zcytor1.  
XX  
KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;  
XX cancer diagnosis; agonist; antagonist; alternatively spliced.  
XX Homo sapiens.  
XX  
PN WO9744455-A1.  
XX  
PD 27-NOV-1997.  
XX  
PF 19-MAY-1997; 97WO-US008502.  
XX  
PR 23-MAY-1996; 96US-00653740.  
XX (ZYMO ) ZYMOGENETICS INC.  
PA Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;  
PI  
XX  
XX  
DR WPI; 1998-018509/02.  
DR N-PSDB; AAT94120.  
XX  
PT Haematopoietic cytokine receptor - useful for ligand detection, and  
XX pathological condition diagnosis.  
PS Claim 7; Page 46-51; 86pp; English.  
XX  
CC The present sequence is an alternatively spliced human haematopoietic  
CC cytokine receptor Zcytor1, useful for ligand detection, and pathological  
CC condition diagnosis, including cancer. Receptor agonists of the protein  
CC immunosuppression, e.g. viral infections. They may also be used to  
CC cells in vitro and in vivo. The agonists can stimulate cell mediated  
CC immunity and lymphocyte proliferation, to treat infection involving  
CC suppress tumours, induce cytotoxicity, treat leukopaenias and enhance the  
CC regeneration of the T-cell repertoire after bone marrow transplantation.  
CC Antagonists of the protein may be used to suppress the immune system,  
CC treat autoimmune diseases, including rheumatoid arthritis, multiple  
CC sclerosis and diabetes mellitus. Immune suppression caused by the  
CC antagonists can also be used to reduce rejection of tissue or organ

CC transplants and grafts, and to treat T-cell specific leukaemias and  
CC lymphomas  
XX  
SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 2; Length 636;  
Best Local Similarity 100.0%; Pred. No. 8.1e-265;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPLKALLPLWLVLFQRTPOGSAGPLQCYGVGGLDNCSEWPLGDL 60  
DB 1 MRGGRGAPFWLWPLKALLPLWLVLFQRTPOGSAGPLQCYGVGGLDNCSEWPLGDL 60

QY 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGOPLPVPFV 120  
DB 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGOPLPVPFV 120

QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180  
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180

QY 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
DB 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240

QY 241 NLCGTPGGEEPLLWKAPGCVQVSKVWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300  
DB 241 NLCGTPGGEEPLLWKAPGCVQVSKVWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300

QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVAGSTELLVTWQPGGEPLEHVVDWARDGD 360  
DB 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVAGSTELLVTWQPGGEPLEHVVDWARDGD 360

QY 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420  
DB 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420

QY 421 TLWRLQDAPPGTPIAWGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSQNTQSVTLPLD 480  
DB 421 TLWRLQDAPPGTPIAWGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSQNTQSVTLPLD 480

QY 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540  
DB 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540

QY 541 RCYHLRHVKVLPWVWEKVPDPANSSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPPVMESS 600  
DB 541 RCYHLRHVKVLPWVWEKVPDPANSSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPPVMESS 600

RESULT 2

AAG65270  
ID AAG65270 standard; protein; 636 AA.  
XX  
AC AAG65270;  
XX  
DT 20-NOV-2001 (first entry)  
DE  
DE Cell factor receptor CRL1.  
XX  
XX Cell factor receptor; CRL1; gpl30; cancer; inflammation;  
KW immunological rejection.  
XX  
XX Unidentified.  
XX  
XX CN1299828-A.  
XX  
PD 20-JUN-2001.  
XX

PF 16-DEC-1999; 99CN-00124269.  
XX  
PR 16-DEC-1999; 99CN-00124269.  
XX  
PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.  
XX  
PI Cao X, Zhang W, He L;  
XX  
DR WPI; 2001-523189/58.  
DR N-PSDB; AAH79286.  
XX  
PT New cell factor acceptor, its code sequence and use.  
XX  
PS Claim 1; Page 19; 27pp; Chinese.  
XX  
CC The present invention provides the protein and coding sequences of a  
CC novel cell factor receptor, designated CRL1. This is a homogeneous  
CC molecule of gpl30. The sequences can be used in the treatment of cancer,  
CC inflammation and immunological rejection. The present sequence is the  
CC protein of the invention  
XX  
SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 4; Length 636;  
Best Local Similarity 100.0%; Pred. No. 8.1e-265;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPLKALLPLWLVLFQRTPOGSAGPLQCYGVGGLDNCSEWPLGDL 60  
DB 1 MRGGRGAPFWLWPLKALLPLWLVLFQRTPOGSAGPLQCYGVGGLDNCSEWPLGDL 60

QY 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGOPLPVPFV 120  
DB 61 GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLLVWGTKAGOPLPVPFV 120

QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180  
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRQCEAAWTLLE 180

QY 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
DB 181 PELKTIPLTPVEIQDELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240

QY 241 NLCGTPGGEEPLLWKAPGCVQVSKVWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300  
DB 241 NLCGTPGGEEPLLWKAPGCVQVSKVWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300

QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVAGSTELLVTWQPGGEPLEHVVDWARDGD 360  
DB 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVAGSTELLVTWQPGGEPLEHVVDWARDGD 360

QY 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420  
DB 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVTAVSAGSLASASSVWGFREELAPLVGP 420

QY 421 TLWRLQDAPPGTPIAWGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSQNTQSVTLPLD 480  
DB 421 TLWRLQDAPPGTPIAWGEVPRHQLRGLHTHYTLCAQSGTSPSCMVNVSQNTQSVTLPLD 480

QY 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540  
DB 481 PWGCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540

QY 541 RCYHLRHVKVLPWVWEKVPDPANSSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPPVMESS 600  
DB 541 RCYHLRHVKVLPWVWEKVPDPANSSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPPVMESS 600

QY 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636  
DB 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636



QY 481 PWGCELWWTASTIAGQPPGILRLHLPDNTLRWKLPGILFLWGLFLGGLSLATSG 540  
 DB 481 PWGCELWWTASTIAGQPPGILRLHLPDNTLRWKLPGILFLWGLFLGGLSLATSG 540  
 QY 541 RCYHLRHKVLPRWWEKVPDPANSSGGQPHMBQVPEAQPLGLDLPILEVEEMPPPPVMESS 600  
 DB 541 RCYHLRHKVLPRWWEKVPDPANSSGGQPHMBQVPEAQPLGLDLPILEVEEMPPPPVMESS 600  
 QY 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636  
 DB 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 4  
 ADD68151  
 ID ADD68151 standard; protein; 636 AA.  
 XX AC  
 XX ADD68151;  
 DT 15-JAN-2004 (first entry)  
 XX Human WSX-1 receptor polypeptide SEQ ID NO:9.  
 DE human; zcytor17; antiinflammatory; dermatological; immunosuppressive;  
 KW antimicrobial; vaccine; inflammatory disease; inflammatory bowel disease;  
 KW ulcerative colitis; Crohn's disease; atopic dermatitis; eczema;  
 KW psoriasis; endotoxaemia; septicemia; toxic shock syndrome;  
 KW infectious disease.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2003060090-A2.  
 PN  
 XX 24-JUL-2003.  
 PD  
 XX 21-JAN-2003; 2003WO-US001984.  
 PF  
 XX 18-JAN-2002; 2002US-0350325P.  
 PR 25-APR-2002; 2002US-0375323P.  
 PR 19-DEC-2002; 2002US-0435315P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Sprecher CA, Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;  
 PI Novak JE, Gross JA, Dillon SR;  
 PI  
 XX WPI; 2003-618179/59.  
 DR N-PSDB; ADD68150.  
 DR  
 XX New zcytor17 ligand polypeptides, useful for treating inflammatory  
 PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's  
 PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.  
 XX Example 3; SEQ ID NO 9; 372pp; English.  
 XX The invention relates to a novel isolated zcytor17 ligand polypeptide. A  
 CC polypeptide of the invention has antiinflammatory, dermatological, and  
 CC immunosuppressive, and antimicrobial activity, and may have a use in a  
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,  
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
 CC shock syndrome or infectious diseases. The present sequence is used in  
 CC the exemplification of the invention.  
 XX  
 XX Sequence 636 AA;  
 SQ

Query Match 100.0%; Score 3498; DB 7; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 8,1e-265;  
 Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPLPKLALLPVLFWLFTQTRPQGSAGPLQCYGVGFLGDLNCSWEPLGDL 60  
 61 GAPSELHQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLWGTGKAGOPLPWPPFV 120  
 61 GAPSELHQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLWGTGKAGOPLPWPPFV 120  
 121 NLETQMKFNAPRLGPDVDFSEDDPLEATVHWAPTPWPSHKVLIQCFHYRRCOEAAWTLLE 180  
 121 NLETQMKFNAPRLGPDVDFSEDDPLEATVHWAPTPWPSHKVLIQCFHYRRCOEAAWTLLE 180  
 181 PELKTIPLTPVEIQDLELATGYKYVGRCKMEKEDLWGEWSPILSFQPPAPKDVWVSG 240  
 181 PELKTIPLTPVEIQDLELATGYKYVGRCKMEKEDLWGEWSPILSFQPPAPKDVWVSG 240  
 241 NLCGTPGGEELPILLWKAPGPCVQVSYKWFVWVGRELSPEGITCCCSLIPSGAEWARVSA 300  
 241 NLCGTPGGEELPILLWKAPGPCVQVSYKWFVWVGRELSPEGITCCCSLIPSGAEWARVSA 300  
 301 VNATSWPELTNLSLVCLDSASAPRSVAVSSVSIAGSTELLVTWQPGEPLEHVVDWARDGD 360  
 301 VNATSWPELTNLSLVCLDSASAPRSVAVSSVSIAGSTELLVTWQPGEPLEHVVDWARDGD 360  
 361 PLEKLNWVRLPPGNLSALLPGNFTVGVYRITVTAVSASGLASASSVWGFEEELAPLYGP 420  
 361 PLEKLNWVRLPPGNLSALLPGNFTVGVYRITVTAVSASGLASASSVWGFEEELAPLYGP 420  
 421 TLMRLQDAPPGTPTAANGEVPRHQLRHGLTHYTLCAQSGTSPSVCMNVSGNTQSVTLTDL 480  
 421 TLMRLQDAPPGTPTAANGEVPRHQLRHGLTHYTLCAQSGTSPSVCMNVSGNTQSVTLTDL 480  
 481 PWGCELWWTASTIAGQPPGILRLHLPDNTLRWKLPGILFLWGLFLGGLSLATSG 540  
 481 PWGCELWWTASTIAGQPPGILRLHLPDNTLRWKLPGILFLWGLFLGGLSLATSG 540  
 541 RCYHLRHKVLPRWWEKVPDPANSSGGQPHMBQVPEAQPLGLDLPILEVEEMPPPPVMESS 600  
 541 RCYHLRHKVLPRWWEKVPDPANSSGGQPHMBQVPEAQPLGLDLPILEVEEMPPPPVMESS 600  
 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636  
 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 5  
 ADL26574  
 ID ADL26574 standard; protein; 636 AA.  
 XX AC  
 XX ADL26574;  
 DT 20-MAY-2004 (first entry)  
 XX Human WSX-1 receptor.  
 DE  
 XX antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;  
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;  
 KW immune response inhibitor; inflammatory response inhibitor;  
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;  
 KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;  
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;  
 KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;  
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;  
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;  
 KW septicemia; toxic shock syndrome; zcytor17lig; human; receptor;  
 KW zcytor17 ligand; WSX-1 receptor; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003215838-A1.  
 XX 20-NOV-2003.  
 PD  
 XX 21-JAN-2003; 2003US-00351157.  
 PF  
 XX



PR 18-JAN-2002; 2002US-0350325P.  
PR 14-JUN-2002; 2002US-0389108P.  
PR 19-DEC-2002; 2002US-0435361P.  
XX (SPRE/) SPRECHER C A.  
PA (GAOZ/) GAO Z.  
PA (KUIJ/) KUIJPER J L.  
PA (DASO/) DASOVICH M M.  
PA (GRAN/) GRANT F J.  
PA (PRES/) PRESNELL S R.  
PA (WHIT/) WHITMORE T E.  
PA (HAMW/) HAMMOND A K.  
PA (NOVA/) NOVAK J E.  
PA (GROS/) GROSS J A.  
PA (DILL/) DILLON S R.  
XX  
PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ;  
PI Presnell SR, Whitmore TE, Hammond AX, Novak JE, Gross JA, Dillon SR;  
XX  
DR WPI; 2003-876545/81.  
DR N-PSDB; ADL26573.  
XX  
XX Novel multimeric or heterodimeric cytokine receptors useful for treating  
PT chronic inflammatory disease such as inflammatory bowel disease,  
PT ulcerative colitis, acute inflammatory disease such as endotoxemia,  
PT septicemia.  
XX  
PS Example 3; SEQ ID NO 9; 205pp; English.  
XX  
CC The invention describes an isolated multimeric or heterodimeric cytokine  
CC receptor (I) having at least one polypeptide having 90 percent sequence  
CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in  
CC specification, and where (I) binds a ligand comprising a 164 (S3) amino  
CC acid sequence, given in specification, or at least one polypeptide  
CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells  
CC and producing an antibody to (I) and a cytokine-binding domain of a class  
CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-  
CC binding domain of a class I cytokine receptor and a vehicle is useful  
CC for: reducing haematopoietic cells and hematopoietic progenitor cells in  
CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation  
CC of hematopoietic cells and hematopoietic progenitor cells; reducing  
CC zcytor17lig-induced inflammation; treating a mammal afflicted with an  
CC inflammatory disease in which zcytor17lig plays a role. The disease is a  
CC chronic inflammatory disease such as inflammatory bowel disease,  
CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and  
CC psoriasis. The disease is acute inflammatory disease such as  
CC endotoxaemia, septicaemia, toxic shock syndrome and infectious disease.  
CC An immune response inhibiting composition is useful for inhibiting an  
CC immune response in a mammal exposed to an antigen or pathogen. An  
CC inflammatory response inhibiting composition is useful for suppressing an  
CC inflammatory response in a mammal with inflammation. An antibody that  
CC specifically binds to (I) is useful for detecting the presence of a  
CC multimeric or heterodimeric cytokine receptor in a biological sample.  
CC This is the amino acid sequence of a human WSX-1 receptor used in the  
CC creation of a vector expressing full length zcytor17.  
XX  
SQ Sequence 636 AA;  
Query Match 100.0%; Score 3498; DB 7; Length 636;  
Best Local Similarity 100.0%; Pred. No. 8.1e-265;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRGRGAPFWLWLPKLLALLPLLVLFQRTVRPGSAGPLQCYGVGVLGDLNCSWEPLGDL 60  
DB 1 MRGRGAPFWLWLPKLLALLPLLVLFQRTVRPGSAGPLQCYGVGVLGDLNCSWEPLGDL 60  
QY 61 GAPSELHLSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLLVMGTAKGQPLWPPVFV 120  
DB 61 GAPSELHLSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLLVMGTAKGQPLWPPVFV 120  
QY 121 NLETOMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQBAATLLE 180  
DB 121 NLETOMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQBAATLLE 180

QY 181 PELKTIPLTPVEIQDLELATGYKYGRCRMKEEDLWGWSPILSFQTPPSAPKDVWVSG 240  
DB 181 PELKTIPLTPVEIQDLELATGYKYGRCRMKEEDLWGWSPILSFQTPPSAPKDVWVSG 240  
QY 241 NLCGTPGGEPEPLLLWKAPGCVQVSKVWFVWVGRELSPGEGITCCCSLLIPSGAEWAVSA 300  
DB 241 NLCGTPGGEPEPLLLWKAPGCVQVSKVWFVWVGRELSPGEGITCCCSLLIPSGAEWAVSA 300  
QY 301 VNATSWEPITNLISLVCLDSASAPRSVAVSSVAGSTELLVTWQPGPGLHVVDWARDGD 360  
DB 301 VNATSWEPITNLISLVCLDSASAPRSVAVSSVAGSTELLVTWQPGPGLHVVDWARDGD 360  
QY 361 PLEKLNWVRLPPGNLSALLPGNFTVGVPRYRITTVAVSASGLASASSVWGFREELAPLVGP 420  
DB 361 PLEKLNWVRLPPGNLSALLPGNFTVGVPRYRITTVAVSASGLASASSVWGFREELAPLVGP 420  
QY 421 TLWRLQDAPPGTAPAIANGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLPLDL 480  
DB 421 TLWRLQDAPPGTAPAIANGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLPLDL 480  
QY 481 PMGFCELWVTASTIAGQPGPILRLHLPDNTLRWKVLPGLILFWGLFLGCGLSLATSG 540  
DB 481 PMGFCELWVTASTIAGQPGPILRLHLPDNTLRWKVLPGLILFWGLFLGCGLSLATSG 540  
QY 541 RCVHLRHKVLPRVWVEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVPPVMESS 600  
DB 541 RCVHLRHKVLPRVWVEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVPPVMESS 600  
QY 601 QPAQATAPLDGSGYEKHFILPTPEELGLLGP RPQVLA 636  
DB 601 QPAQATAPLDGSGYEKHFILPTPEELGLLGP RPQVLA 636  
RESULT 6  
ADU91801  
ID ADL91801 standard; protein; 636 AA.  
XX  
AC ADL91801;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human PRO34336 protein SEQ ID NO:22.  
XX  
KW human; PRO; immune related disease; immunosuppressive; dermatological;  
KW hepatotropic; nephrotropic; antidiabetic; antiaesthetic; antipsoriatic;  
KW antiallergic; antianemic; antiarteriosclerotic; antiarthritic;  
KW neuroprotective; respiratory; antiinflammatory; gene therapy;  
KW immune related disorder; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
KW spondyloarthritis; systemic sclerosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome;  
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;  
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;  
KW immune-mediated renal disease; demyelinating disease;  
KW idiopathic demyelinating polyneuropathy; Guillain-Barré syndrome;  
KW chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;  
KW infectious hepatitis; autoimmune chronic active hepatitis;  
KW primary biliary cirrhosis; granulomatous hepatitis;  
KW sclerosing cholangitis; inflammatory bowel disease;  
KW gluten-sensitive enteropathy; Whipple's disease;  
KW immune-mediated skin disease; bullous skin disease; erythema multiforme;  
KW contact dermatitis; psoriasis; allergic disease; asthma;  
KW allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;  
KW immunologic disease; eosinophilic pneumonia;  
KW idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;  
KW transplantation associated disease; graft rejection;  
XX graft-versus-host-disease.  
OS Homo sapiens.  
XX  
PN W02004024076-A2.  
XX

PD 25-MAR-2004.  
 XX 10-SEP-2003; 2003WO-US028361.  
 XX 11-SEP-2002; 2002US-0410174P.  
 XX (GETH ) GENENTECH INC.  
 XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;  
 PI Williams FM, Wood WI, Wu TD;  
 XX WPI; 2004-269874/25.  
 DR N-PSDB; ADL91800.  
 XX New PRO nucleic acid useful for preparing a composition for diagnosing or  
 PT treating an immune related disorder, e.g., systemic lupus erythematosus  
 PT in a mammal.  
 XX Claim 10; SEQ ID NO 22; 200pp; English.  
 XX The present invention describes isolated nucleic acid sequences encoding  
 CC novel proteins (PRO), which can be used in the treatment of immune  
 CC related diseases. The PRO sequences have immunosuppressive,  
 CC dermatological, hepatotropic, nephrotropic, antidiabetic, antiaesthatic,  
 CC antipsoriatic, antiallergic, antianaemic, antiarteriosclerotic,  
 CC antiarthritic, neuroprotective, respiratory and antiinflammatory  
 CC activities, and can be used in gene therapy. The PRO nucleic acids or  
 CC proteins can be used for preparing a composition for diagnosing or  
 CC treating an immune related disorder, e.g., systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,  
 CC myopathy, Sjogren's syndrome, systemic sclerosis, idiopathic inflammatory  
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis,  
 CC diabetes mellitus, immune-mediated renal disease, a demyelinating disease  
 CC of the central or peripheral nervous system, idiopathic demyelinating  
 CC demyelinating polyneuropathy, hepatobiliary disease, infectious or  
 CC polynuropathy, Guillain-Barre syndrome, chronic inflammatory  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or  
 CC immune-mediated skin disease, bullous skin disease, erythema multiforme,  
 CC contact dermatitis, psoriasis, allergic disease, asthma, allergic  
 CC rhinitis, atopic dermatitis, food hypersensitivity, urticaria,  
 CC immunologic disease of the lung, eosinophilic pneumonia, idiopathic  
 CC pulmonary fibrosis, hypersensitivity pneumonitis, transplantation  
 CC associated disease, graft rejection or graft-versus-host-disease. The  
 CC present sequence represents a novel human PRO protein from the present  
 CC invention.  
 XX Sequence 636 AA;  
 SQ  
 Query Match 100.0%; Score 3498; DB 8; Length 636;  
 Best Local Similarity 100.0%; Fred. No. 8.1e-265;  
 Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRGGRGAPFWLPLKLLALLLWLVLFQTRPQSGAGPLQCYGVGVLGDLNCSWEPLGDL 60  
 DB 1 MRGGRGAPFWLPLKLLALLLWLVLFQTRPQSGAGPLQCYGVGVLGDLNCSWEPLGDL 60  
 QY 61 GAPSELHLSQKYSRKNKTQVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFV 120  
 DB 61 GAPSELHLSQKYSRKNKTQVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVFV 120  
 QY 121 NLETKMKNAPRLGDVDFSEDDPLEATVHVAAPPTWPSHKVLICOPHYRRCOEAAWTLLE 180  
 DB 121 NLETKMKNAPRLGDVDFSEDDPLEATVHVAAPPTWPSHKVLICOPHYRRCOEAAWTLLE 180  
 QY 181 PELKTIPTLPVBIQDELATGKYVGRCEMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
 DB 181 PELKTIPTLPVBIQDELATGKYVGRCEMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
 QY 241 NLCGTPGGEPELLLWKAPGCPQVSYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 DB 241 NLCGTPGGEPELLLWKAPGCPQVSYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300

DB 241 NLCGTPGGEPELLLWKAPGCPQVSYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 QY 301 VNATSWPEPLTNLSLVCLDSASAPRSVAVSSYTAGSTELLVWQPGCEPLEHVVDWARDGD 360  
 DB 301 VNATSWPEPLTNLSLVCLDSASAPRSVAVSSYTAGSTELLVWQPGCEPLEHVVDWARDGD 360  
 QY 361 PLEKLNWVRLPPGNLSALLPGNFTVGVPRITVTAVSASGLASASSVWGFEELAPLVGP 420  
 DB 361 PLEKLNWVRLPPGNLSALLPGNFTVGVPRITVTAVSASGLASASSVWGFEELAPLVGP 420  
 QY 421 TLWRLQDAPPPTPAIANGVEVPRHQLRGLHLYTICAQSGTSPSCMVNVSQVTLPLDL 480  
 DB 421 TLWRLQDAPPPTPAIANGVEVPRHQLRGLHLYTICAQSGTSPSCMVNVSQVTLPLDL 480  
 QY 481 PWGPCELWVTASTTAGCGPPGPIRLRLHLPDNTLRKWLPGILFLWGLFLLGGLSLATSG 540  
 DB 481 PWGPCELWVTASTTAGCGPPGPIRLRLHLPDNTLRKWLPGILFLWGLFLLGGLSLATSG 540  
 QY 541 RYHLRHKVLPRVWWEKVPDPANSSSGQPHMEQVPEAQPLGDLPILEVEEMPPVPMESS 600  
 DB 541 RYHLRHKVLPRVWWEKVPDPANSSSGQPHMEQVPEAQPLGDLPILEVEEMPPVPMESS 600  
 QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
 DB 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
 RESULT 7  
 ADRI4163  
 ID ADRI4163 standard; protein; 636 AA.  
 XX ADRI4163;  
 AC ADRI4163;  
 XX 21-OCT-2004 (first entry)  
 DT Human NF-kappaB pathway-associated protein SeqID164.  
 XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
 KW antiarthritic; antieumatic; gastrointestinal-Gen; antiaesthatic;  
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
 KW immunosuppressive; vulnery; gene therapy; immune disorder;  
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
 KW rheumatoid arthritis; host cell survival; evasion of immune response;  
 KW atherosclerosis; cachexia; inflammatory bowel disease; colitis; asthma;  
 KW autoimmune disorder; hyper immune activity;  
 KW aberrant acute phase response; hypercongenital condition; birth defect;  
 KW necrotic lesion; wound; organ transplant rejection;  
 KW aberrant signal transduction; proliferating disorder; cancer;  
 KW HIV propagation; human.  
 XX Homo sapiens.  
 XX WO2004065577-A2.  
 XX 05-AUG-2004.  
 XX 13-JAN-2004; 2004WO-US000798.  
 XX 14-JAN-2003; 2003US-0440068P.  
 XX 12-MAY-2003; 2003US-0469757P.  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;  
 XX WPI; 2004-562168/54.  
 XX N-PSDB; ADRI4162.  
 XX

PT New isolated polynucleotides and polypeptides associated with NF-kappaB  
PT pathway, useful for diagnosing, treating, or preventing disorders or  
PT diseases associated with NF-kappaB pathway.  
XX  
PS Claim 6; SEQ ID NO 164; 237pp; English.  
XX  
CC This invention relates to the novel association of protein sequences (and  
CC the genes which encode them) to the NF-kappaB pathway. The invention may  
CC be useful for the production of compounds with an anti-inflammatory,  
CC cycostatic, hepatotropic, virucide, antiarthritic, antiinflammatory,  
CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,  
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
CC vulnary activity or for gene therapy. The proteins and nucleotides are  
CC useful for diagnosing, preventing, treating, or ameliorating conditions  
CC or diseases associated with the NF-kappaB pathway. The condition is an  
CC immune disorder, an inflammatory disorder, an inflammatory disorder  
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic  
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
CC immune activity, disorders related to aberrant acute phase responses,  
CC - hypercongenital conditions, birth defects, necrotic lesions, wounds,  
CC organ transplant rejection, conditions related to organ transplant  
CC rejection, disorders related to aberrant signal transduction,  
CC proliferating disorders, cancers and HIV propagation in cells infected  
CC with other viruses. The present sequence is that of a human protein which  
CC is subject to the novel association with the NF-kappaB pathway of the  
CC invention. Note: This sequence does not appear in the specification but  
CC was obtained by the indexer from Genbank.

XX SQ Sequence 636 AA;

Query Match 100.0%; Score 3498; DB 8; Length 636;  
Best Local Similarity 100.0%; Pred. No. 8.1e-265;  
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGRGPFLLWPKLALLPLLVLFQRTFPGSAGPLQCYGVGLDNCSEWPLGDL 60  
DB 1 MRGGRGPFLLWPKLALLPLLVLFQRTFPGSAGPLQCYGVGLDNCSEWPLGDL 60  
QY 61 GAPSGLHQSOKYRSNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKQPLWPFV 120  
DB 61 GAPSGLHQSOKYRSNTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKQPLWPFV 120  
QY 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180  
DB 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRCQEAATLLE 180  
QY 181 PELKTIPLTVEIQDLATGKYVGRCEKEEDLWGEWSPILSFQTPPSAPKDVWWSG 240  
DB 181 PELKTIPLTVEIQDLATGKYVGRCEKEEDLWGEWSPILSFQTPPSAPKDVWWSG 240  
QY 241 NLCTPGGEPFLWAPGPCVQVYKFWVWVGRELSPGICITCCSLIPSGAEWAVSA 300  
DB 241 NLCTPGGEPFLWAPGPCVQVYKFWVWVGRELSPGICITCCSLIPSGAEWAVSA 300  
QY 301 VNATSWEPFLNLSVCLDSASAPRSVAVSSITAGSTELLVWQPGFPLEHVVDWARDGD 360  
DB 301 VNATSWEPFLNLSVCLDSASAPRSVAVSSITAGSTELLVWQPGFPLEHVVDWARDGD 360  
QY 361 PLEKLNWRLPPGNLSALLPQNFVTPYRITVAVSAGSLASASSWGFRRELAPLVGP 420  
DB 361 PLEKLNWRLPPGNLSALLPQNFVTPYRITVAVSAGSLASASSWGFRRELAPLVGP 420  
QY 421 TLWLQDAPCTPAIANGEVPRHOLRGHLTHYTLCAQSGTSPSCVMVNSGNTQSVTLPLD 480  
DB 421 TLWLQDAPCTPAIANGEVPRHOLRGHLTHYTLCAQSGTSPSCVMVNSGNTQSVTLPLD 480  
QY 481 PWGPELWVTASTIAGQPGPILRLHLPNTLRLWKVLPGLFLWGLFLLGCGLSLATSG 540

DB 481 PWGPELWVTASTIAGQPGPILRLHLPNTLRLWKVLPGLFLWGLFLLGCGLSLATSG 540  
QY 541 RCYHLRHKVLPRVWKEVPDPANSSSQPHMEQVPEAQPLGDLPILEVEWEPVNVSS 600  
DB 541 RCYHLRHKVLPRVWKEVPDPANSSSQPHMEQVPEAQPLGDLPILEVEWEPVNVSS 600  
QY 601 QPAQATAPLDSGYEKHFLPTPEELGLLGP RPQVLA 636  
DB 601 QPAQATAPLDSGYEKHFLPTPEELGLLGP RPQVLA 636

RESULT 8  
ABG32294

ID ABG32294 standard; protein; 636 AA.

XX AC ABG32294;

XX DT 10-DEC-2002 (first entry)

XX DE Human IL-12R-like subunit protein.

XX KW IL-D80; human; cytokine; anti-inflammatory; haematopoietic; interleukin;  
XX IL-27; haematopoietic cell; immune system; inflammation;  
XX KW IL-12R-like subunit; interleukin 12 receptor like subunit.

XX OS Homo sapiens.

XX PN WO200268596-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-US005493.

XX PR 22-FEB-2001; 2001US-00791497.

XX PR 30-NOV-2001; 2001US-00000776.

XX PA (SCHE ) SCHERING CORP.

XX PI Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;

XX PI Dewaal Malefyt R, Cheung J;

XX DR WPI; 2002-706978/76.

XX DR N-PSDB; ABS54548.

XX PT New polynucleotide and its encoded antigenic polypeptide (IL-D80

PT cytokine), useful for regulating hematopoietic cells, in developing new  
PT therapies, or for diagnosing or treating abnormal physiology, e.g.  
PT inflammations.

XX PS Claim 24; Page 72-74; 74pp; English.

XX CC This invention relates to the DNA and protein sequences of a new cytokine  
CC IL-D80. The protein of the invention may have antiinflammatory activity  
CC and may act as an IL-D80 modulator or an IL-27 modulator. The  
CC polynucleotide of the invention or its encoded polypeptide is useful for  
CC regulating the activation, development, differentiation or function of  
CC various cell types, e.g. haematopoietic cells. This polynucleotide or  
CC polypeptide is also useful in discovering and developing new lymphokines  
CC and their related receptor or receptor subunits, and in developing new  
CC therapies for a wide range of degenerative or abnormal conditions, which  
CC (in)directly involve the immune system or haematopoietic cells. The  
CC polynucleotide or polypeptide is useful in diagnosing or treating  
CC abnormal physiology or development, e.g. inflammations. The present  
CC sequence represents the human interleukin 12- receptor-like subunit  
CC protein of the invention

XX SQ Sequence 636 AA;

Query Match 99.9%; Score 3494; DB 5; Length 636;  
Best Local Similarity 99.8%; Pred. No. 1.7e-264;  
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPKLALLPLLVLFQRTTRPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60  
 DB 1 MRGGRGAPFWLWPKLALLPLLVLFQRTTRPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60  
 QY 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVNGTKAGOPLPVPPV 120  
 DB 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVNGTKAGOPLPVPPV 120  
 QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180  
 DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180  
 QY 181 PELKTIPLTPVEIQDELELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPPAPKDVWVSG 240  
 DB 181 PELKTIPLTPVEIQDELELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPPAPKDVWVSG 240  
 QY 241 NLCGTPGGEPEPLLWKAPGCVQVSKYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 DB 241 NLCGTPGGEPEPLLWKAPGCVQVSKYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPEPLEHVVDWARDGD 360  
 DB 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPEPLEHVVDWARDGD 360  
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVAVSAGSLASASVWGFREELAPLVGP 420  
 DB 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVAVSAGSLASASVWGFREELAPLVGP 420  
 QY 421 TLWRLQDAPPGTPTAANGVPRHQRGLHLYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480  
 DB 421 TLWRLQDAPPGTPTAANGVPRHQRGLHLYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480  
 QY 481 PWGPCELWVTASTIAGQGGPGLRLHLPDNTLRWKVLPGLFLMGLFLGCGLSLATSG 540  
 DB 481 PWGPCELWVTASTIAGQGGPGLRLHLPDNTLRWKVLPGLFLMGLFLGCGLSLATSG 540  
 QY 541 RCYHLRHKVLPKRWVWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVWESS 600  
 DB 541 RCYHLRHKVLPKRWVWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVWESS 600  
 QY 601 QPAQATAPLDSGYEKHFLPTPELGLLGPVLA 636  
 DB 601 QPAQATAPLDSGYEKHFLPTPELGLLGPVLA 636

RESULT 9  
 ABU09752  
 ID ABU09752 standard; protein; 636 AA.  
 AC ABU09752;  
 XT 07-JUL-2003 (first entry)  
 DE Human T-cell cytokine receptor (TCR).  
 KW Human; interleukin; IL-D80; IL-D80; DNAX; immunosuppressive;  
 KW antiinflammatory; cardiant; nootropic; neuroprotective; gene therapy;  
 KW antigen; cell activation; cell development; cell differentiation;  
 KW haematopoietic cell; immune disorder; T-cell immune deficiency;  
 KW inflammation; tissue rejection; cardiovascular disorder; TCCR;  
 KW neurophysiological condition; immunological condition; receptor;  
 KW Epstein barr virus induced gene 3; EB13; T-cell cytokine receptor.  
 OS Homo sapiens.  
 XX US2003008343-A1.  
 PN 09-JAN-2003.  
 PD 22-FEB-2001; 2001US-00791497.  
 PF 30-JUL-1999; 99US-0146581P.  
 PR 06-AUG-1999; 99US-0147763P.

PR 27-JUL-2000; 2000US-00627897.  
 XX (TIMA/) TIMANS J C.  
 PA (PFLA/) PFLANZ S K.  
 PA (KAST/) KASTELEIN R A.  
 PA (BAZA/) BAZAN J F.  
 XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF;  
 XX WPI; 2003-428883/40.  
 DR N-PSDB; ACA61018.  
 XX New substantially pure or isolated antigenic polypeptide that binds to  
 PT the binding composition, useful for treating immune disorders, e.g. T-  
 PT cell immune deficiencies, inflammation, tissue rejection, or  
 PT cardiovascular conditions.  
 XX Disclosure; Page 31-32; 39pp; English.  
 XX The invention describes a substantially pure or isolated antigenic  
 CC polypeptide, which binds to the binding composition comprising at least  
 CC 17 contiguous amino acids from a sequence of 242, 231, 243 or 234 amino  
 CC acids, fully defined in specification. The polynucleotides, polypeptides  
 CC and antibodies are useful for regulating activation, development,  
 CC differentiation, and functions of various cell types, including  
 CC haematopoietic cells. They are also useful for treating abnormal medical  
 CC conditions, including immune disorders, e.g. T-cell immune deficiencies,  
 CC inflammation, tissue rejection, or cardiovascular or neurophysiological  
 CC conditions. The antibodies are useful for detecting or diagnosing various  
 CC immunological conditions related to expression of respective antigens.  
 CC This is the amino acid sequence of human T-cell cytokine receptor (TCCR)  
 CC to which the composite factor formed by IL-D80 and Epstein barr virus  
 CC induced gene-3 (EB13) binds  
 XX Sequence 636 AA;  
 SQ Query Match 99.9%; Score 3494; DB 6; Length 636;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-264;  
 Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGGRGAPFWLWPKLALLPLLVLFQRTTRPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60  
 DB 1 MRGGRGAPFWLWPKLALLPLLVLFQRTTRPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60  
 QY 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVNGTKAGOPLPVPPV 120  
 DB 61 GAPSELHLOSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVNGTKAGOPLPVPPV 120  
 QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180  
 DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLE 180  
 QY 181 PELKTIPLTPVEIQDELELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPPAPKDVWVSG 240  
 DB 181 PELKTIPLTPVEIQDELELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPPAPKDVWVSG 240  
 QY 241 NLCGTPGGEPEPLLWKAPGCVQVSKYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 DB 241 NLCGTPGGEPEPLLWKAPGCVQVSKYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPEPLEHVVDWARDGD 360  
 DB 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPEPLEHVVDWARDGD 360  
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVAVSAGSLASASVWGFREELAPLVGP 420  
 DB 361 PLEKLNWVRLPGNLSALLPGNFTVGPYRITVAVSAGSLASASVWGFREELAPLVGP 420  
 QY 421 TLWRLQDAPPGTPTAANGVPRHQRGLHLYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480  
 DB 421 TLWRLQDAPPGTPTAANGVPRHQRGLHLYTLCAQSGTSPSCVMNVSNGTQSVTLPLD 480  
 QY 481 PWGPCELWVTASTIAGQGGPGLRLHLPDNTLRWKVLPGLFLMGLFLGCGLSLATSG 540

Db 481 PWGCELVWTASTTAGQPPGPIRLHLDPDNTLRKWLPGILFLWGLFLGCGSLATSG 540  
Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600  
Db 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600  
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636  
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 10  
ID ABG75880 standard; protein; 636 AA.  
XX AC ABG75880;  
XX DT 06-MAY-2003 (first entry)  
XX Human interleukin-12 R beta 2 subunit homologue WSX-1/TCR.  
XX DE Human; cytokine; IL-D80; IL-27; interleukin D80; interleukin 27;  
XX inflammation; autoimmune disorder; drug screening; cell activation;  
XX cell development; cell differentiation; WSX-1/TCR;  
XX interleukin-12 R beta 2 subunit.  
XX OS Homo sapiens.  
XX PN US2002164609-A1.  
XX PD 07-NOV-2002.  
XX PF 30-NOV-2001; 2001US-00000776.  
XX PR 30-JUL-1999; 99US-0146581P.  
XX PR 06-AUG-1999; 99US-0147763P.  
XX PR 27-JUL-2000; 2000US-00627897.  
XX PR 22-FEB-2001; 2001US-00791497.  
XX (TIMA/) TIMANS J C.  
XX (PFLA/) PFLANZ S K.  
XX (KAST/) KASTELEIN R A.  
XX (BAZA/) BAZAN J F.  
XX (RENN/) RENNICK D.  
XX (WALE/) DE WAAL MALEFYT R.  
XX (CHEU/) CHEUNG J.  
XX Timans JC, Pflanz SK, Kastelein RA, Bazan JF, Rennick D;  
XX De Waal Malefyt R, Cheung J;  
XX WPI; 2003-275305/27.  
XX N-PSDB; ABX10922.  
XX New isolated or recombinant cytokine or composite cytokine genes and  
XX proteins (e.g. interleukin D80 or interleukin 27), useful for diagnosing  
XX or treating e.g. inflammation or autoimmune disorders, or for regulating  
XX cell biology.  
XX Claim 24; Page 30-32; 37pp; English.  
XX The invention describes an isolated or recombinant polynucleotide, which  
XX encodes an antigenic polypeptide. The polynucleotide, polypeptide or  
XX binding compound is useful for diagnosing or treating IL-D80 or IL-27  
XX mediated conditions, e.g. inflammation or autoimmune disorders. These are  
XX also useful in drug screening. The polynucleotide, polypeptide,  
XX antibodies or compositions are also useful for controlling biology and  
XX physiology of mammalian cells (e.g. cells of a mammalian immune system),  
XX or for regulating the activation, development, differentiation, and  
XX function of various cell types (e.g. hematopoietic or lymphoid cells).  
XX This is the amino acid sequence of the human interleukin-12 R beta 2  
XX subunit homologue WSX-1/TCR used with human interleukin D80 (IL-D80) or  
XX 27 (IL-27) sequences to create a composite cytokine

XX SQ Sequence 636 AA;  
Query Match 99.9%; Score 3494; DB 6; Length 636;  
Best Local Similarity 99.8%; Pred. No. 1.7e-264;  
Matches 636; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MRGGRGAPFWLWPLPKLALLPLLLWVLFQRTTRPGSAGPLQCYGVGPIGLDNCSEWPLGDL 60  
Db 1 MRGGRGAPFWLWPLPKLALLPLLLWVLFQRTTRPGSAGPLQCYGVGPIGLDNCSEWPLGDL 60  
Qy 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKQPLWPPVVF 120  
Db 61 GAPSELHLSQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTGKQPLWPPVVF 120  
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLLICQFYHRCQEAATLLE 180  
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLLICQFYHRCQEAATLLE 180  
Qy 181 PELKTIPLTPEVEIQDLELATGYKYVYGRCKMEKEEDLWGEWSPILSFOTPPSAPKDVVWSG 240  
Db 181 PELKTIPLTPEVEIQDLELATGYKYVYGRCKMEKEEDLWGEWSPILSFOTPPSAPKDVVWSG 240  
Qy 241 NLCGTPGGEERPLLWKAPGCVQVYKVPWFVWGRELSPEGITCCCSLIPSGAEWAVSA 300  
Db 241 NLCGTPGGEERPLLWKAPGCVQVYKVPWFVWGRELSPEGITCCCSLIPSGAEWAVSA 300  
Qy 301 VNATSWEPILTNLSIVCLDSASAPRSVAVSSIASTELLVTWQPGEPLEHVVDWARDGD 360  
Db 301 VNATSWEPILTNLSIVCLDSASAPRSVAVSSIASTELLVTWQPGEPLEHVVDWARDGD 360  
Qy 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITTVAVSASGLASSVWGFREELAPLVGP 420  
Db 361 PLEKLNWRLPPGNLSALLPGNFTVGVYRITTVAVSASGLASSVWGFREELAPLVGP 420  
Qy 421 TLWRLQDAPGTPAIANGVEVPRHLRGHLTHYLCAQSGTSPSYCMNVSGNTQVTLPLDL 480  
Db 421 TLWRLQDAPGTPAIANGVEVPRHLRGHLTHYLCAQSGTSPSYCMNVSGNTQVTLPLDL 480  
Qy 481 PWGCELVWTASTTAGQPPGPIRLHLDPDNTLRKWLPGILFLWGLFLGCGSLATSG 540  
Db 481 PWGCELVWTASTTAGQPPGPIRLHLDPDNTLRKWLPGILFLWGLFLGCGSLATSG 540  
Qy 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600  
Db 541 RCYHLRHKVLPRVWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVPMVSS 600  
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636  
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636

RESULT 11  
AA29781  
ID AAY29781 standard; protein; 636 AA.  
XX AC AAY29781;  
XX DT 04-NOV-1999 (first entry)  
XX DE Human DNAX cytokine receptor subunit 1.  
XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
XX interleukin B30; DSR81; IL-B30; cytokine receptor; diagnosis;  
XX inflammatory disorder; inflammatory response; innate immunity;  
XX morphogenic development; immunological disorder.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
XX FH Misc-difference 108 /label= unknown  
XX FT /note= "encoded by AYT"

XX WO940195-A1.  
 PN 12-AUG-1999.  
 PD 05-FEB-1999; 99WO-US002600.  
 PF 06-FEB-1998; 98US-0073941P.  
 PR 13-MAY-1998; 98US-00078194.  
 XX (SCHE) SCHERING CORP.  
 PA Matteson JD, Mcclanahan TK, Kastelein RA;  
 PI WPI; 1999-527306/44.  
 DR N-PSDB; AA208863.  
 DR  
 XX New receptor subunits useful in the treatment inflammatory disorders.  
 PT Claim 2; Page 14-17; 133pp; English.  
 PS  
 XX The present invention describes a composition (I) comprising DNAX  
 CC cytokine receptor subunit 1 (DCRS1) protein and DNAX soluble receptor  
 CC subunit 1 (DSRS1) protein, which together encode a new mammalian cytokine  
 CC related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or  
 CC DRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1 is useful for  
 CC screening for ligands (i.e. agonists/antagonists) from a library of  
 CC compounds, which are useful for modulating the physiology or development  
 CC of a cell or tissue culture e.g. inflammatory responses, innate immunity  
 CC and/or morphogenic development. (R), antibodies and ligands are useful  
 CC for treatment of conditions, especially immunological disorders,  
 CC associated with conditions exhibiting abnormal expression of (R). (R) is  
 CC useful as a phosphate labeling enzyme to label substrates, and the  
 CC subunits DRS1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding  
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from  
 CC other individuals or species. The present sequence represents the  
 CC specifically claimed human DCRS1, for use in the composition of the  
 CC present invention  
 XX Sequence 636 AA;  
 SQ  
 Query Match 99.8%; Score 3490; DB 2; Length 636;  
 Best Local Similarity 99.7%; Pred. No. 3.4e-264;  
 Matches 634; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MRGGRGAPFWLWPLPKALLLLVLFQRTTRQGSAGPLQCYGVGGLDNCWEPLGDL 60  
 DB 1 MRGGRGAPFWLWPLPKALLLLVLFQRTTRQGSAGPLQCYGVGGLDNCWEPLGDL 60  
 QY 61 GAPSELHLOQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTKAGQPLWPPVSV 120  
 DB 61 GAPSELHLOQKYSRNTQTVAAGRSWVAIPREQLTMSDKLLVWGTXKAGQPLWPPVSV 120  
 QY 121 NLEQTMKPNAPRLGPDVDFSEDDPLEATVHVAAPPTWPSHKVLICQPHYRRCQEAATLLE 180  
 DB 121 NLEQTMKPNAPRLGPDVDFSEDDPLEATVHVAAPPTWPSHKVLICQPHYRRCQEAATLLE 180  
 QY 181 PELKTIPLTPVEIQDLELATGVKRCMEKEEDLWGEWSPILSQTTPPSAPKDVWVSG 240  
 DB 181 PELKTIPLTPVEIQDLELATGVKRCMEKEEDLWGEWSPILSQTTPPSAPKDVWVSG 240  
 QY 241 NLGCTPGGEEPLLWKAPGCVQVSVKVFVWVGRELSPGEGITCCCSLLIPSGAEARVSA 300  
 DB 241 NLGCTPGGEEPLLWKAPGCVQVSVKVFVWVGRELSPGEGITCCCSLLIPSGAEARVSA 300  
 QY 301 VNATSWEPITNLSVLCDLSASAPRSVAVSSIAGSTELLVTWQPGGEPLEHVVDWARDGD 360  
 DB 301 VNATSWEPITNLSVLCDLSASAPRSVAVSSIAGSTELLVTWQPGGEPLEHVVDWARDGD 360  
 QY 361 PLEKLNWVRLPPGNLSALLPGNFTVGPYRITVTVASGLASASVWGFRELAPLVGP 420  
 DB 361 PLEKLNWVRLPPGNLSALLPGNFTVGPYRITVTVASGLASASVWGFRELAPLVGP 420

QY 421 TLWRLQDAPPCTPAIANGVEVPRHQLRGLHLYTLCAQSGTSPSVCMNVSGNTQSVTLPLD 480  
 DB 421 TLWRLQDAPPCTPAIANGVEVPRHQLRGLHLYTLCAQSGTSPSVCMNVSGNTQSVTLPLD 480  
 QY 481 PWGPCELWVTASTIAGQPPGPPIRLHLDPNTLWKVLPGLFLWGLFLGCGLSLATSG 540  
 DB 481 PWGPCELWVTASTIAGQPPGPPIRLHLDPNTLWKVLPGLFLWGLFLGCGLSLATSG 540  
 QY 541 RCYHLRHVKVLPWWWEKVPDPANSSSGOPHMEQVPEAQLGDLPLILEVEEMEPVPMWESS 600  
 DB 541 RCYHLRHVKVLPWWWEKVPDPANSSSGOPHMEQVPEAQLGDLPLILEVEEMEPVPMWESS 600  
 QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
 DB 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636

RESULT 12  
 AAG65271  
 ID AAG65271 standard; protein; 604 AA.  
 AC AAG65271;  
 XX 20-NOV-2001 (first entry)  
 DT Cell factor receptor CRL1 related protein.  
 DE Cell factor receptor CRL1 related protein.  
 XX Cell factor receptor; CRL1; gpi30; cancer; inflammation;  
 KW immunological rejection.  
 XX Unidentified.  
 OS CN1299828-A.  
 PN 20-JUN-2001.  
 PD 16-DEC-1999; 99CN-00124269.  
 PF 16-DEC-1999; 99CN-00124269.  
 PR 16-DEC-1999; 99CN-00124269.  
 XX (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.  
 PA Cao X, Zhang W, He L;  
 PI WPI; 2001-523189/58.  
 DR New cell factor acceptor, its code sequence and use.  
 XX Example 1; Page 19; 27pp; Chinese.  
 CC The present invention provides the protein and coding sequences of a  
 CC novel cell factor receptor, designated CRL1. This is a homogeneous  
 CC molecule of gpi30. The sequences can be used in the treatment of cancer,  
 CC inflammation and immunological rejection. The present sequence is a  
 CC protein described in the exemplification of the invention  
 XX Sequence 604 AA;  
 SQ  
 Query Match 94.8%; Score 3316; DB 4; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-250;  
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 33 QGSAGPLQCYGVGGLDNCWEPLGDLGAPSELHLOQKYSRNTQTVAAGRSWVAI 92  
 DB 1 QGSAGPLQCYGVGGLDNCWEPLGDLGAPSELHLOQKYSRNTQTVAAGRSWVAI 60  
 QY 93 PREQLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNAPRLGPDVDFSEDDPLEATVHVA 152  
 DB 61 PREQLTMSDKLLVWGTKAGQPLWPPVFNLETQMKPNAPRLGPDVDFSEDDPLEATVHVA 120  
 QY 153 PPTWPSHKVLICQPHYRRCQEAATLLEPLKTIPLTPVEIQDLELATGVKRCMEK 212







Db 310 YKWFVWVGRELSPEGITCCSLIPSGAEWARVSAVNATSWEBTLNLSLVCLDSASAPRS 369  
 QY 326 VAVSSITAGTELLVTWQPGPGPLEHVVDWARDGPLEKLNWRLLPPGNLSALLPGNFV 385  
 Db 370 VAVSSITAGTELLVTWQPGPGPLEHVVDWARDGPLEKLNWRLLPPGNLSALLPGNFV 429  
 QY 386 GVPYRITVAVSAGSLASASSVWGPREELAPLVGPTLWRLQDAPCTPAIANGVEPRHQL 445  
 Db 430 GVPYRITVAVSAGSLASASSVWGPREELAPLVGPTLWRLQDAPCTPAIANGVEPRHQL 489  
 QY 446 RGHLYTLCAQSGTSPSCVMNVSGNTQSVTLTDLPMWGPCELWVTASTIAGQPGPIIL 505  
 Db 490 RGHLYTLCAQSGTSPSCVMNVSGNTQSVTLTDLPMWGPCELWVTASTIAGQPGPIIL 549  
 QY 506 LHLPDNTLRWLVKVLPGILFLWGLFLGCGLSLATSRCYHLRHKVLPRWWEKVPDPANSS 565  
 Db 550 LHLPDNTLRWLVKVLPGILFLWGLFLGCGLSLATSRCYHLRHKVLPRWWEKVPDPANSS 609  
 QY 566 SGQPMQEQVPEAQLGDLPLILEVEEMEPVPMVMESSQPAQATAPLDSGYEKHFLPTPEILG 625  
 Db 610 SGQPMQEQVPEAQLGDLPLILEVEEMEPVPMVMESSQPAQATAPLDSGYEKHFLPTPEILG 669  
 QY 626 LLGPPRPQVLA 636  
 Db 670 LLGPPRPQVLA 680

RESULT 14

AAW33398  
 ID AAW33398 standard; protein; 578 AA.  
 AC AAW33398;  
 DT 22-MAY-1998 (first entry)  
 DE Human haematopoietic cytokine receptor Zcytor1.  
 KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;  
 KW cancer diagnosis; agonist; antagonist.  
 OS Homo sapiens.  
 PN WO9744455-A1.  
 PD 27-NOV-1997.  
 PF 19-MAY-1997; 97WO-US008502.  
 PR 23-MAY-1996; 96US-00653740.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;  
 DR WPI; 1998-018509/02.  
 DR N-PSDB; AAT94119.  
 PT Haematopoietic cytokine receptor - useful for ligand detection, and  
 PT pathological condition diagnosis.  
 PS Claim 1; Page 39-43; 86pp; English.

CC The present sequence is the human haematopoietic cytokine receptor  
 CC Zcytor1, useful for ligand detection, and pathological condition  
 CC diagnosis, including cancer. Receptor agonists of the protein can be used  
 CC to stimulate the proliferation and development of target cells in vitro  
 CC and in vivo. The agonists can stimulate cell mediated immunity and  
 CC lymphocyte proliferation, to treat infection involving immunosuppression,  
 CC e.g. viral infections. They may also be used to suppress tumours, induce  
 CC cytotoxicity, treat leukaemia and enhance the regeneration of the T-  
 CC cell repertoire after bone marrow transplantation. Antagonists of the  
 CC protein may be used to suppress the immune system, treat autoimmune  
 CC diseases, including rheumatoid arthritis, multiple sclerosis and diabetes

CC mellitis. Immune suppression caused by the antagonists can also be used  
 CC to reduce rejection of tissue or organ transplants and grafts, and to  
 XX treat T-cell specific leukaemias and lymphomas  
 SQ Sequence 578 AA;  
 Query Match 90.1%; Score 3150; DB 2; Length 578;  
 Best Local Similarity 90.9%; Pred. No. 1.2e-237;  
 Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;  
 QY 1 MRGGRGAPFWLWPKLALLPLLVLFORTRPGSAGPLQCYGVGPGDLNCSWEPLGDL 60  
 Db 1 MRGGRGAPFWLWPKLALLPLLVLFORTRPGSAGPLQCYGVGPGDLNCSWEPLGDL 60  
 QY 61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLPPV 120  
 Db 61 GAPSELHLQSKYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKGQPLPPV 120  
 QY 121 NLETQMKENAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCOEAAWTLLE 180  
 Db 121 NLETQMKENAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLIQCFHYRRCOEAAWTLLE 180  
 QY 181 PELKTIPLTPVEIODLELATGKVVYGRCKMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
 Db 181 PELKTIPLTPVEIODLELATGKVVYGRCKMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240  
 QY 241 NLGCTPGGEEPLLWKAAPGCVQVSKYKWFVWVGRELSPEGITCCSLIPSGAEWARVSA 300  
 Db 241 NLGCTPGGEEPLLWKAAPGCVQVSKYKWFVWVGRELSPEGITCCSLIPSGAEWARVSA 300  
 QY 301 VNATSWEPDLNLSVCLDSASAPRSVAVSSITAGTELLVTWQPGPELEHVVDWARDGD 360  
 Db 301 VNATSWEPDLNLSVCLDSASAPRSVAVSSITAGTELLVTWQPGPELEHVVDWARDGD 360  
 QY 361 PLEKLNWVRLPPGNLSALLPGNFVTVAVSAGSLASASSVWGPREELAPLVGP 420  
 Db 361 PLEKLNWVRLPPGNLSALLPGNFVTVAVSAGSLASASSVWGPREELAPLVGP 420  
 QY 421 TLWRLQDAPCTPAIANGVEPRHQLRHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLTDL 480  
 Db 421 TLWRLQDAPCTPAIANGVEPRHQLRHLTHYTLCAQSGTSPSCVMNVSGNTQSVTLTDL 480  
 QY 481 PWGPELWVTASTIAGQPGPIILRLHPDNTLRWLVKVLPGILFLWGLFLGCGLSLATS 540  
 Db 481 PWGPELWVTASTIAGQPGPIILRLHPDNTLRWLVKVLPGILFLWGLFLGCGLSLATS 540  
 QY 541 RCYHLRHKVLPRWWEKVPDPANSSSQPMHNEQVPEAQLGDLPLILEVEEMEPVPMVMESS 600  
 Db 541 RCYHLRHKVLPRWWEKVPDPANSSSQPMHNEQVPEAQLGDLPLILEVEEMEPVPMVMESS 600  
 QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636  
 Db 567 -----GLLGPPRPQVLA 578

RESULT 15

ADO26826  
 ID ADO26826 standard; protein; 558 AA.  
 XX ADO26826;  
 AC ADO26826;  
 DT 12-AUG-2004 (first entry)  
 DE Human receptors and membrane-associated protein, REMAP-16.  
 KW Human; receptors and membrane-associated protein; REMAP;  
 KW cell proliferative disorder; autoimmune disorder; inflammatory disorder;  
 KW neurological disorder; infection; developmental disorder;  
 KW nervous system disorder; mental disorder; metabolic disorder;  
 KW hepatotropic; antipariatic; nontropic; neuroprotective;  
 KW antiparkinsonian; anticonvulsant; anorectic; osteopathic;  
 KW hypertensive; anti-HIV; antiaesthetic; antianaemic; ophthalmological;  
 KW thrombolytic; anticoagulant.

XX	Homo sapiens.	
OS	WO2004044159-A2.	
XX	27-MAY-2004.	
XX	10-NOV-2003; 2003WO-US035752.	
XX	12-NOV-2002; 2002US-0425404P.	
PR	15-JAN-2003; 2003US-0440907P.	
PR	24-JAN-2003; 2003US-0442477P.	
PR	18-FEB-2003; 2003US-0448585P.	
PR	04-APR-2003; 2003US-0460716P.	
PR	09-APR-2003; 2003US-0461853P.	
XX	(INCY-) INCYTE CORP.	
XX	Lee SY, Swarnakar A, Murage J, Khare R, Hafalia AJA, Chawla NK; PI Elliott VS, Tran UK, Becha SD, Bhatia U, Burrill JD, Lee S; PI Blake JJ, Ho A, Zheng W, Marquis JP, Jin P, Wilson AD, Wang JT; PI Chien D, Richardson TW, Kable AE, Emerling BM, Ramkumar J; PI Baughn MR, Tang YT, Jackson JL, Lal PG, Yue H, Gietzen KJ; XX WPI; 2004-420303/39.	
DR	N-PSDB; ADO26875.	
XX	Novel isolated human receptors and membrane-associated proteins, REMAP 1-49, useful for diagnosing, treating, preventing AIDS, obesity, hypothyroidism, acromegaly, cataract, thrombosis, Alzheimer's disease.	
XX	Claim 1; SEQ ID NO 16; 292pp; English.	
XX	The present invention relates to the isolation of human receptors and membrane-associated proteins (REMAP, designated REMAP-1 to REMAP-49), and the polynucleotide sequences encoding them. Also disclosed are expression vectors, host cells, antibodies, agonists, and antagonists. The polypeptide and polynucleotide sequences of the invention are useful for diagnosing, treating, and preventing disorders associated with aberrant expression of REMAP. Such disorders include cell proliferative disorders, autoimmune disorders, inflammatory disorders, neurological disorders, infections, developmental disorders, nervous system disorders, mental disorders, metabolic disorders etc. The present sequence represents a REMAP polypeptide of the invention.	
XX	Sequence 558 AA;	

Search completed: February 19, 2005, 01:12:54  
Job time : 179 secs

Query Match	86.0%;	Score 3007;	DB 8;	Length 558;
Best Local Similarity	87.4%;	Pred. No. 1.9e-226;		
Matches 556;	Conservative 1;	Mismatches 1;	Indels 78;	Gaps 1;
Qy	1	MRGGRGPFWLWPLPKLALLPLLVLFORTPOGSAGPLOCYGVGGLDNCSEWPLGDL	60	
Db	1	MRGGRGPFWLWPLPKLALLPLLVLFORTPOGSAGPLOCYGVGGLDNCSEWPLGDL	60	
Qy	61	GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLIVMGTKAGQPLWPPFV	120	
Db	61	GAPSELHLQSKYRSNKTQTVAAAGRSWVAIPREQLTMSDKLIVMGTKAGQPLWPPFV	120	
Qy	121	NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAANTLLE	180	
Db	121	NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAANTL--	178	
Qy	181	PELXTIPLTPVETQDLATGKYVYGRCKREKEEDLNGEWSPILSFQTTPSAPKDVWWSG	240	
Db	179	-----	178	
Qy	241	NLCGTPGGEPELLWLLKAPGCVQYSYKVFVWGRELSPGICCCSLIPSGAEWARVSA	300	
Db	179	-----APGPCVQYSYKVFVWGRELSPGICCCSLIPSGAEWARVSA	222	
Qy	301	VNATSWEPPLTNLSIVCLDSASAPRSVAVSISAGSTELLVTWQPGPGEPLHVVVDWARDGD	360	

Db	223	VNATSWEPPLTNLSIVCLDSASAPRSVAVSISAGSTELLVSWQPGPGEPLHVVVDWARDGD	282	
Qy	361	PLEKLNWVRLPPCGNLGALLPGNFTVGVYRITVTAVSASGLASASSVWGFREELAPLVGP	420	
Db	283	PLEKLNWVRLPPCGNLGALLPGNFTVGVYRITVTAVSASGLASASSVWGFREELAPLVGP	342	
Qy	421	TLWRLQDAPPGTPTAIANGEVPRHQLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL	480	
Db	343	TLWRLQDAPPGTPTAIANGEVPRHQLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL	402	
Qy	481	PWGPCELWVTASTIAGOGPGPILRLHLDPNTLRWKVLPGLILFWGLFLGCGLSLATS	540	
Db	403	PWGPCELWVTASTIAGOGPGPILRLHLDPNTLRWKVLPGLILFWGLFLGCGLSLATS	462	
Qy	541	RCYHLRHKVLPRVWVEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMERPPVWMESS	600	
Db	463	RCYHLRHKVLPRVWVEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMERPPVWMESS	522	
Qy	601	QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA	636	
Db	523	QPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA	558	

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